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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2001, 06:56:33 : Search time 2376.51 Seconds
(Without alignments)
138.835 Million cell updates/sec

Title: US-09-800-629a-52

Perfect score: 1 tttctcagtcacagttgt 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 541028

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 33: em_hlg_hum:*
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- 35: em_hlg_inv:*
- 36: em_hlg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	24	6	AR6923
3	20	100.0	24	6	AR048335
4	20	100.0	24	6	AR079226
5	14.4	72.0	24	6	128768
6	14.4	72.0	24	6	170526
7	13.4	67.0	25	6	A22036
8	13.4	67.0	43	6	AX167229
9	13.4	67.0	48	6	E15948
10	13.2	66.0	34	6	AR074516
11	13.2	66.0	16	6	172347
12	12.8	64.0	17	6	172348
13	12.8	64.0	17	6	AX045082
14	12.8	64.0	27	6	AX148237
15	12.8	64.0	29	6	A35733
16	12.6	63.0	29	6	AR007315
17	12.6	63.0	29	6	176376
18	12.6	63.0	31	6	AR022300
19	12.6	63.0	40	6	A35734
20	12.6	63.0	41	6	A23270
21	12.6	63.0	41	6	152201
22	12.6	62.0	25	6	A57414
23	12.4	62.0	25	6	AR131459
24	12.4	62.0	27	6	A47990
25	12.4	62.0	27	6	AX190998
26	12.4	62.0	18	11	HSY19RAP1
27	12.2	61.0	24	6	AR051748
28	12.2	61.0	24	6	AR051748
29	12.2	61.0	32	6	A87189
30	12.2	61.0	33	6	AX000844
31	12.2	61.0	42	6	AR021377
32	12.2	61.0	42	6	AR042939
33	12.2	61.0	42	6	143928
34	12.2	61.0	42	6	162930
35	12.2	61.0	42	6	186683
36	12.2	61.0	22	6	AX003318
37	12.2	60.0	22	6	AR149556
38	12.2	60.0	41	6	AR077632
39	12.2	60.0	41	6	AR077633
40	12.2	60.0	41	6	AR077634
41	12.2	60.0	44	6	AR034442
42	12.2	60.0	44	6	AR070387
43	12.2	60.0	45	6	AR099087
44	12.2	60.0	45	6	AR099116
45	12.2	60.0	45	6	AR099116

ALIGNMENTS

RESULT 1

AR136249 AR136249 20 bp DNA

LOCUS Sequence 52 from patent US 6136603.

DEFINITION AR136249

ACCESSION AR136249

VERSION AR136249.1 GI:14476421

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dean,N.M., Karras,J.G., and McKay,R.

TITLE Antisense modulation of interleukin-5 signal transduction

JOURNAL Patent: US 6136603-A 52 24-OCT-2000;

FEATURES

Source Location/Qualifiers

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BASE COUNT 3 a 4 c 5 g 8 t

PAT 16-JUN-2001

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Db 1 TTCTTCAGTCACAGTTGCT 20

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LOCUS AR6923 24 bp DNA PAT 22-JAN-2000
DEFINITION Sequence 14 from patent WO9838306.
ACCESSION AR6923
VERSION AR6923.1 GI:6735707

KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 24)

AUTHORS Dolganov, G.
TITLE TRANSCRIPTS ENCODING IMMUNOMODULATORY POLYPEPTIDES
JOURNAL Patent: WO 9838306-A 14 03-SEP-1998;
GENELABS TECH INC (US)

FEATURES
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Location/Qualifiers

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RESULT 3

LOCUS AR048335 24 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5821091
ACCESSION AR048335
VERSION AR048335.1 GI:5970678

KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)

AUTHORS Dolganov, G.
TITLE Method of identifying activated T-cells
JOURNAL Patent: US 5821091-A 14 13-OCT-1998;
FEATURES
source 1..24
Location/Qualifiers

BASE COUNT 9 a 7 c 4 g 4 t
ORIGIN
/organism="unknown"

Query Match 100.0%; Score 20; DB 6; Length 24;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 TTCTTCAGTCACAGTTGCT 2

RESULT 4
LOCUS AR079226 24 bp DNA PAT 31-AUG-2000
DEFINITION Sequence 14 from patent US 5965427.
ACCESSION AR079226
VERSION AR079226.1 GI:10005971

KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)

AUTHORS Dolganov, G. and Novikov, A.
TITLE Human RAD50 gene and methods of use thereof
JOURNAL Patent: US 5965427-A 14 12-OCT-1999;
FEATURES
source 1..24
Location/Qualifiers

BASE COUNT 9 a 7 c 4 g 4 t
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/organism="unknown"

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Db 21 TTCTTCAGTCACAGTTGCT 2

RESULT 5

LOCUS 128768 24 bp DNA PAT 06-FEB-1997
DEFINITION Sequence 3 from patent US 5573939.
ACCESSION 128768
VERSION 128768.1 GI:1819544

KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)

AUTHORS B.ang.vik.C.O., Eriksson, U. and Peterson, P.A.
TITLE DNA encoding mammalian retinol binding protein receptor, and
JOURNAL corresponding vectors and transformed cells
PATENT: US 5573939-A 3 12-NOV-1996;
FEATURES
source 1..24
Location/Qualifiers

BASE COUNT 9 a 5 c 7 g 3 t
ORIGIN
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Db 18 TCAGTCACAGTTGCT 3

RESULT 6

LOCUS 170526 24 bp DNA PAT 03-APR-1998
DEFINITION Sequence 3 from patent US 5679772.
ACCESSION 170526
VERSION 170526.1 GI:3006661

KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)

AUTHORS B.ang.vik.C.Olof, Eriksson, U. and Peterson, P.A.

TITLE Mammalian retinol-binding protein receptors
JOURNAL Patent: US 5679772-A 3 21-OCT-1997;
FEATURES Location/Qualifiers
source 1..24
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 tcagtcacagcttgc 20
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Db 18 TCAGTCACAGCTGCT 3

RESULT 7
LOCUS A22036.25 bp DNA PAT 04-OCT-1994
DEFINITION Oligonucleotide P4.
ACCESSION A22036
VERSION A22036.1 GI:641411
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 25)
AUTHORS Sonigo, P., Brechot, C. and Cournaud, V.
TITLE Oligonucleotide sequences for amplification of type HIV-2 and siv
retroviruses genomes and their application to in-vitro diagnostic
of infections caused by these viruses
Patent: EP 0404625-A 12 27-DEC-1990;
JOURNAL INSTITUT PASTEREUR; INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE
MEDICALE (INSERM)
FEATURES Location/Qualifiers
source 1..25
/organism="synthetic construct"
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 24 CTTAGTCACAGCTGC 8

RESULT 8
LOCUS AX167229 43 bp DNA PAT 03-JUL-2001
DEFINITION Sequence 8 from Patent WO0142463.
ACCESSION AX167229
VERSION AX167229.1 GI:14596696
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 43)
AUTHORS Lu, J. and Wlitcher, D.R.
TITLE Improving stability of flint through o-linked glycosylation
JOURNAL Patent: WO 0142463-A 8 14-JUN-2001;
FEATURES Location/Qualifiers
source 1..43
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligo primer"

BASE COUNT 13 a 11 c 14 g 5 t
ORIGIN

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Best Local Similarity 93.3%; Pred. No. 6.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ttctcagtcacag 15
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Db 9 TTCATCAGTCACAG 23

RESULT 9
LOCUS E15948.48 bp DNA PAT 28-JUL-1999
DEFINITION Primer.
ACCESSION E15948
VERSION E15948.1 GI:5710631
KEYWORDS JP 1998113191-A/27.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 48)
AUTHORS Ishimura, M. and Nishigaki, T.
TITLE HUMAN INTERFERON TAU VARIANT
JOURNAL Patent: JP 1998113191-A 27 06-MAY-1998;
SANKYO CO LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1998113191-A/27
PD 06-MAY-1998
PF 20-AUG-1997 JP 199722318
PR 21-AUG-1996 JP 96P 219879
PI ISHIMURA MASAKO, NISHIGAKI TAKASHI
PC C12N15/09, A61K38/21, A61K38/21, C07H21/04, C07K14/555,
PC C12P21/02, (C12N1/21, C12R1:19), (C12P21/02, C12R1:19); CC
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CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH key
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Db 40 CAGTCACAGCTGCT 26

RESULT 10
LOCUS A79313 34 bp DNA PAT 20-OCT-1999
DEFINITION Sequence 1 from Patent WO9804706.
ACCESSION A79313
VERSION A79313.1 GI:6092357
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified
unclassified.

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REFERENCE 1 (bases 1 to 34)
AUTHORS Connor,S.E. and Whittle,N.R.
TITLE POLYPEPTIDES USEFUL AS IMMUNOTHERAPEUTIC AGENTS AND METHODS OF
JOURNAL POLYPEPTIDE PREPARATION
PATENT: WO 9804706-A 1 05-FEB-1998;
FEATURES
SOURCE location/Qualifiers
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Best Local Similarity 83.3%; Pred. No. 8.8e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 tcttcagtcacagctgg 19
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Db 13 TCTTCGCTGCCACATGC 30

RESULT 11
LOCUS AR074516 34 bp DNA PAT 28-AUG-2000
DEFINITION Sequence 1 from patent US 5955087:
ACCESSION AR074516
VERSION AR074516.1 GI:10001271
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 34)
AUTHORS Whittle,N.Richard, Carmichael,J.Paddon, Connor,S.Edward,
Thompson,H.Stephengrammer and Wilson,M.Jonathan.
TITLE Polypeptides useful as immunotherapeutic agents and methods of
JOURNAL Polypeptide preparation
PATENT: US 5955087-A 1 21-SEP-1999;
FEATURES
SOURCE location/Qualifiers
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/db_xref="taxon:32644"
BASE COUNT 6 a 8 c 13 g 7 t
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Db 13 TCTTCGCTGCCACATGC 30

RESULT 12
LOCUS I72347 16 bp DNA PAT 03-APR-1998
DEFINITION Sequence 3 from patent US 5683902.
ACCESSION I72347
VERSION I72347.1 GI:3008486
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Hampel,A., DiPaolo,J., Siwkowski,A.M. and Galasinski,S.C.
TITLE Human papilloma virus inhibition by a hairpin ribozyme
JOURNAL Patent: US 5683902-A 3 04-NOV-1997;
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SOURCE location/Qualifiers
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BASE COUNT 5 a 3 c 4 g 4 t
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ORIGIN

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Db 16 TTCTTCAGACACAGT 1

RESULT 13
LOCUS I72348 17 bp DNA PAT 03-APR-1998
DEFINITION Sequence 4 from patent US 5683902.
ACCESSION I72348
VERSION I72348.1 GI:3008487
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Hampel,A., DiPaolo,J., Siwkowski,A.M. and Galasinski,S.C.
TITLE Human papilloma virus inhibition by a hairpin ribozyme
JOURNAL Patent: US 5683902-A 4 04-NOV-1997;
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Db 16 TTCTTCAGACACAGT 1

RESULT 14
LOCUS AX045082 20 bp DNA PAT 24-NOV-2000
DEFINITION Sequence 12 from Patent WO0066149.
ACCESSION AX045082
VERSION AX045082.1 GI:11343681
KEYWORDS
SOURCE Synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gerhardt,C., Romero-Romero,I.A. and Strosberg,A.D.
TITLE Medicines useful for treating disorders of regulation of body
fatness and diseases related to disorders of leptin production
JOURNAL Patent: WO 0066149-A 12 09-NOV-2000;
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SOURCE location/Qualifiers
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DB 16 TTCTTCAGCGCACACT 1

RESULT 15

AXI48237/c

AXI48237 27 bp DNA

PAT 08-JUN-2001

DEFINITION Sequence 78 from Patent WO0136471.

ACCESSION AXI48237

VERSION AXI48237.1 GI:14347135

KEYWORDS

SOURCE

ORGANISM

synthetic construct.

synthetic construct

artificial sequence.

1 (bases 1 to 27)

REFERENCE Chen, R., Dang, H.T. and Lowitz, K.P.

Endogenous and non-endogenous versions of human g protein-coupled

receptors Patent: WO 0136471-A 78 25-MAY-2001;

JOURNAL Arena Pharmaceuticals, Inc. (US)

FEATURES location/Qualifiers

SOURCE

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/db_xref="taxon:32630"

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ORIGIN .

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OY 1 ttcttcagcgccact 16

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Job time: 16637 sec

GenCore version 4.5
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OM nucleic acid - nucleic acid search, using sw model

Run on: December 26, 2001, 08:53:58 ; Search time 706.67 seconds

(without alignments)
24.264 Million cell updates/sec

Title: US-09-800-629a-52

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Scoring table: IDENTITY_NUC
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Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 989696

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	14.4	72.0	24	14	AAO33071 RBP receptor clone
6	13.8	69.0	25	12	AAO33052 P4 primer specific
7	13.8	69.0	44	13	AAO33937 Downstream sequenc
8	13.6	68.0	31	20	AAO33870 HPV-16 inhibitor.
9	13.6	68.0	31	20	AAO33873 HPV-16 inhibitor.
10	13.6	68.0	49	16	AAO75472 HPV primer probe H
11	13.4	67.0	27	18	AAO68145 Human IL1 VEGF re

C	12	13.4	67.0	27	19	AAV55515 Human c-fos hammer
13	13.4	67.0	43	21	AAAB8735 Human FLINT mutagenic PCR prim	
14	13.4	67.0	47	21	AAAB7384 Human map-related PCR primer tau-d1-	
C	15	13.4	67.0	48	20	AAV22976 Human papillomavir
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C	17	13.4	67.0	30	18	AAV59419 Human papillomavir
C	18	13.2	66.0	31	19	AAV67604 Human papillomavir
C	19	13.2	66.0	31	19	AAV38943 Human papillomavir
20	13.2	66.0	34	17	AAV39344 Human papillomavir	
21	13.2	66.0	34	16	AAV15139 Human papillomavir	
22	13.2	66.0	50	16	AAO75488 Human papillomavir	
C	23	13.2	66.0	16	17	AAV40307 HPV-7 E7 gene PCR
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26	12.8	64.0	16	20	AAV33872 HPV-16 inhibitor.	
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32	12.8	64.0	20	19	AAV39225 PCR primer cck77 f	
33	12.8	64.0	20	19	AAZ21983 Mouse caspase 8 mr	
C	34	12.8	64.0	20	22	AAO12418 Human alpha-chemok
C	35	12.8	64.0	20	22	AAO34345 Upstream PCR prime
C	36	12.8	64.0	25	13	AAO34111 Human G-protein co
C	37	12.8	64.0	27	22	AAO75992 AMG variant const
38	12.8	64.0	41	21	AAO75894 Parasitic astacin	
39	12.8	64.0	50	16	AAO75894 Parasitic astacin	
C	40	12.6	63.0	29	17	AAO75894 Parasitic astacin
C	41	12.6	63.0	29	22	AAO11205 D. immitis ndiMPA2
42	12.6	63.0	29	22	AAO11205 RNA polymerase tra	
43	12.6	63.0	31	18	AAO60010 Probe SORF33h 90T	
44	12.6	63.0	31	22	AAO60010 S. venezuelae pik	
45	12.6	63.0	32	21	AAO87312	

ALIGNMENTS

RESULT 1

ID AAC73699 standard; DNA: 20 BP.

XX AAC73699:

XX 02-FEB-2001 (first entry)

XX Human IL-5 antisense oligonucleotide ISIS #16084.

XX Human: interleukin-5; IL-5: signal transduction;

XX antisense oligonucleotide: antiaschmatic; immunosuppressive; cytostatic;

XX IL-5 receptor-alpha; asthma; eosinophilic syndrome; infection;

XX Inflammation; cancer; ss.

XX Homo sapiens.

XX Synthetic.

XX WO200058512-A1.

XX 05-OCT-2000.

XX 17-MAR-2000; 2000WO-US07318.

XX 26-MAR-1999; 99US-0280799.

XX (ISIS-) ISIS PHARM INC.

XX Dean NM, Kattas JG, McKay R;

XX WPI: 2000-594648/56.

XX Antisense oligonucleotide compound used to treat asthma and

XX eosinophilic syndrome in humans modulates interleukin-5 signal

XX

XX

XX

XX

XX

XX

XX

transduction -

Claim 4, Page 63, 156pp; English.

The present sequence is an oligonucleotide used for antisense modulation of interleukin-5 (IL-5) signal transduction. Oligonucleotides were designed to target nucleic acids encoding IL-5 and IL-5 receptor-alpha. The antisense oligonucleotides may be used for the treatment of diseases associated with IL-5 signal transduction, IL-5 expression or IL-5 receptor-alpha expression. Such diseases include asthma and eosinophilic syndrome. The oligonucleotides are also useful for research uses and to prevent or delay infection, inflammation or tumour formation.

Sequence 20 BP; 3 A; 4 C; 5 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ttcttcagtcagcagttgt 20
1 ttcttcagtcagcagttgt 20

RESULT 2
AAV5363/C
ID AAV5363 standard; cDNA; 24 BP.

AAV5363
24-DEC-1998 (first entry)

CDNA synthesis primer IL5-1.

ss: human; RAD50; DNA repair; tumour suppression; cancer; Septin-2; central nervous system; PCR; primer; amplification.

Synthetic.

WO9727284-A2.

31-JUL-1997.

24-JAN-1997; 97WO-US01299.

17-JUL-1996; 96US-0687080.
26-JAN-1996; 96US-0592126.

(GENE-) GENELABS TECHNOLOGIES INC.

Dolganov G;

WPI; 1997-393672/36.

Human tumour suppressor gene RAD50 - useful to detect predisposition to, decrease risk of and treat cancer, also Septin-2 homologues

Example 1; Page 36; 195pp; English.

The primers AAV75354-T75378 were used to for cDNA synthesis in the method of the invention. Disclosed in the invention is human RAD50 (RAD50) which is involved in DNA repair and has tumour suppression activity, and can be used to detect predisposition to, decrease the risk of or treat cancers, e.g. acute myeloid leukaemia, myelodysplastic syndrome, therapy related myelodysplastic syndrome, therapy related acute myeloid leukaemia, refractory anaemia or refractory anaemia with excess blasts. Also disclosed in this invention are human Septin-2 homologues which may be used as targets for cancer therapies and central nervous system directed treatment methods, and to measure the proliferative potential of selected cell types.

Sequence 24 BP; 9 A; 7 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ttcttcagtcagcagttgt 20
21 ttcttcagtcagcagttgt 2

RESULT 3
AAV59945/C
ID AAV59945 standard; DNA; 24 BP.

AAV59945
25-NOV-1998 (first entry)

PCR primer IL5-1 used to amplify interleukin cDNA.

Human analogue; yeast RAD50; Drosophila Septin-2; Acyl-CoA synthetase; immunomodulatory activity; identification; activated T-cell; cytokine; interleukin; IL; PCR primer; ss.

Synthetic.

Homo sapiens.

WO9838306-A1.

03-SEP-1998.

27-FEB-1997; 97WO-US03159.

27-FEB-1997; 97WO-US03159.

(GENE-) GENELABS TECHNOLOGIES INC.

Dolganov G;

WPI; 1998-481207/41.

Novel human immunomodulatory poly(peptide(s) - have homology to the yeast RAD50 or Drosophila Septin-2 proteins

Example 1; Page 27; 155pp; English.

PCR primers AAV59945-46 were used to identify cDNA encoding human cytokine interleukin (IL) from different cDNA pools, to provide an estimate of the degree to which the cytokine transcript is present. mRNA was isolated from activated T-cells, and converted to cDNA prior to amplification. The specification describes sequences encoding human analogues of the yeast RAD50, the Drosophila Septin-2 and Acyl-CoA synthetase. The proteins have immunomodulatory activity. The nucleic acids and proteins can be used to identify activated T-cells in a sample population. They can also be used to isolate and identify sequences encoding other proteins or other compounds having immunomodulatory activity.

Sequence 24 BP; 9 A; 7 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ttcttcagtcagcagttgt 20
21 ttcttcagtcagcagttgt 2


```

RESULT 4
AAI30050/c
ID AAI30050 standard; DNA; 31 BP.
XX
AC AAI30050;
XX
DT 18-OCT-2001 (first entry)
XX
DE Human single nucleotide polymorphism (SNP) HRG 4.
XX
KW Human; resequence; genotype; disease; forensic; paternity testing;
KW single nucleotide polymorphism; SNP; ss.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT Variation replace(16,A)
FT /*tag=
FT /standard_name= "single nucleotide polymorphism"
XX
PD 13-SEP-2001.
XX
PF 07-MAR-2001; 2001MO-US07268.
XX
PR 07-MAR-2000; 2000US-0187510.
PR 22-MAY-2000; 2000US-0206129.
XX
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Cargill M, Ireland JS, Lander ES;
XX
DR WPI: 2001-522952/57.
XX
PT Nucleic acid molecules from the human genome which include polymorphic
PT sites, useful in methods for predicting the presence, absence or
PT severity of a particular phenotype or disorder (e.g. diabetes)
PT associated with a particular genotype -
XX
PS Claim 1: Page 65; 145pp; English.
XX
CC The invention relates to the identification of nucleic acid molecules
CC (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC which can predispose individuals to disease. Various genes from a number
CC of individuals were resequenced and single nucleotide polymorphisms
CC (SNPs) in these genes discovered. The method is useful for predicting the
CC presence, absence or severity of a particular phenotype or disorder (e.g.
CC diabetes) associated with a particular genotype. The nucleic acids
CC containing the polymorphic sites may be useful in forensics and paternity
CC testing.
XX
SQ Sequence 31 BP; 8 A; 12 C; 8 G; 3 T; 0 other:
XX
Query Match 76.0%; Score 15.2; DB 22; Length 31;
Best Local Similarity 85.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 ttcttcagtgcacagttgt 20
DB 28 TTCTTAACTGCCACAGTGT 9

```

```

XX
KW Retinol binding protein; RBP; receptor; retinoid; retinitis;
KW clone; extension; ss.
XX
XX MO9323538-A.
XX
XX 25-NOV-1993.
XX
XX 14-MAY-1993; 93WO-US04586.
XX
XX 15-MAY-1992; 92US-0883539.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX BaviK CO, Eriksson U, Simon A, BaviK C;
XX
XX WPI: 1993-386570/48.
XX
DR
XX
PT New retinol binding protein receptor and homologue coding nucleic
PT acid molecule - useful for diagnosis and treatment of retinoid
PT linked pathological conditions, for hybridisation in stringent
PT conditions and treating retinitis
XX
PS Claim 6: Page 15; 44pp; English.
XX
CC Four extended clones of RBP receptor coding cDNA were isolated.
CC The extensions are given in AAO53071-73 or is the sequence GAGAA.
XX
SQ Sequence 24 BP; 9 A; 5 C; 7 G; 3 T; 0 other:
XX
Query Match 72.0%; Score 14.4; DB 14; Length 24;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 5 tcatgacacagttgt 20
DB 18 TCAGTCACACAGTTGT 3

```

```

RESULT 6
AAO10052/c
ID AAO10052 standard; DNA; 25 BP.
XX
AC AAO10052;
XX
DT 14-MAR-1991 (first entry)
XX
DE P4 primer specific for HIV-2 ROD and SIVmac 142.
XX
KW HIV-2 ROD; SIV mac 142; genomic amplification; ss.
XX
XX WO9015158-A.
XX
XX 13-DEC-1990.
XX
XX 05-JUN-1990; 90MO-FR00394.
XX
XX 02-JUN-1989; 89FR-0007355.
XX
XX (INSP ) INST PASTEUR.
XX
XX (INRM ) INSERM INST NAT SANTE.
XX
XX Sonigo P, Brechot C, Courgnand V;
XX
XX WPI: 1991-007227/01.
XX
DR
XX
PT New oligo-nucleotide primers specific for HIV-2 or SIV mac -
PT useful in genomic amplification of viral nucleic acid before
PT detection by hybridisation test
XX
XX Claim 2: page 19; 32pp; French.
XX

```

CC This primer (claimed) is specific for the fragment of HIV-2 ROD
 CC and SIV mac 142 cDNA covering bases 7782-7805 and 7776-7799 resp.
 CC It is used in a primer pair compsn., e.g. with primer LTR1, to
 CC amplify viral nucleic acid prior to detection using a hybridis-
 CC tion probe.
 CC See also AA010041-51 and AA010053-56.

XX Sequence 25 BP; 6 A; 7 C; 6 G; 6 T; 0 other;

Query Match 69.0%; Score 13.8; DB 12; Length 25;
 Best Local Similarity 88.2%; Pred. No. 5.3e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 ctccagtcacagcttg 19
 ||| ||||| |||
 Db 24 CTTTACGTGCACAGTGG 8

RESULT 7

AA033937
 ID AA033937 standard; DNA; 44 BP.

XX AC AA033937;

DT 02-FEB-1993 (first entry)

XX Downstream sequence of microsatellite from clone TGLA34.

XX PCR: selection; primers: OPTIPRIM; breeding; cattle; parentage;
 XX genetic mapping; traits; amplification; ss.

XX OS Bos taurus.

XX PN WO9213102-A.

XX PD 06-AUG-1992.

XX PF 15-JAN-1992; 92WO-US00340.

XX PR 15-JAN-1991; 91US-0642342.

XX PA (GENM-) GENMARK.

PI Georges M, Massey JM;

DR WPI; 1992-284684/34.

PT Polymorphic bovine DNA markers - used in genetic identification,
 PT gene mapping, and selective breeding

XX Table 7: Page 304; 517pp; English.

CC The sequence is that downstream of a bovine microsatellite sequence
 CC obt'd. by screening a library of bovine MboI DNA fragments of between
 CC 250 and 500 bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe.
 CC One out of 50 clones cross-hybridised. Assuming independent
 CC distribution of microsatellites and MboI sites, the frequency of
 CC (T6)_n >9 microsatellites in the bovine genome is estimated at >100,
 CC 000. The sequence information for ca. 210 such bovine microsatellites
 CC is summarised in the specification and indexed herein (see below).
 CC The sequences upstream and downstream of the microsatellite sequence
 CC were used to generate the required PCR primers for in vitro
 CC amplification of the corresp. microsatellite (using the program
 CC OPTIPRIM). The microsatellites may be used to identify individuals,
 CC for parentage testing, and in the genetic mapping of economic trait
 CC loci or genes involved in the determination of economically important
 CC traits esp. in cattle, to allow selective breeding.
 CC See also AA033501-34437.

XX Sequence 44 BP; 11 A; 13 C; 6 G; 14 T; 0 other;

Query Match 69.0%; Score 13.8; DB 13; Length 44;
 Best Local Similarity 88.2%; Pred. No. 5.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ttcttcagtcacagct 17
 ||||| ||||| |||
 Db 11. ttcttcagtcacagct 27

RESULT 8

AA033870
 ID AA033870 standard; DNA; 31 BP.

XX AC AA033870;

DT 25-JUN-1999 (first entry)

XX HPV-16 inhibitor.

XX HPV-16; inhibitor; antisense oligonucleotide; E6/E7 gene; human;
 XX keratinocyte; cervical cell; cervical tumour; ss.

XX OS Synthetic.

XX PN Human papillomavirus 16.

XX WO913071-A1.

XX PD 18-MAR-1999.

XX PF 03-SEP-1998; 98WO-US18320.

XX PR 05-SEP-1997; 97US-0929140.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Alvarez-Salas L, DiPaolo J;

DR WPI; 1999-243727/20.

PT New antisense oligonucleotide analogs for inhibiting growth of
 PT cervical tumors

XX Claim 4; Page 36; 40pp; English.

CC This sequence represents an antisense oligonucleotide of the invention.
 CC The antisense oligonucleotide analogs (ONS) have a sequence complementary
 CC to a sequence of nucleotides 415-445 of human papilloma virus-16
 CC (HPV-16). The antisense ONS can be used to inhibit expression of HPV gene
 CC E6/E7 in living cells, preferably human keratinocytes or human cervical
 CC cells. They bind to E6/E7 mRNA in the cell, prevent mRNA translation
 CC and promote mRNA degradation by intracellular RNase H. They can be used
 CC for preventing transformation of living cells by HPV. The antisense ONS
 CC are used particularly for inhibiting the growth of cervical tumors.

XX Sequence 31 BP; 8 A; 5 C; 7 G; 11 T; 0 other;

Query Match 68.0%; Score 13.6; DB 20; Length 31;
 Best Local Similarity 80.0%; Pred. No. 6.9e+02;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ttcttcagtcacagctgt 20
 ||||| ||||| |||
 Db 1 ttcttcagtcacagctgt 20

RESULT 9

AA033873
 ID AA033873 standard; RNA; 31 BP.

XX AC AA033873;

DT 25-JUN-1999 (first entry)

```

XX DE HPV-16 inhibitor.
XX XX
XX XX HPV-16: inhibitor; antisense oligonucleotide; E6/E7 gene; human;
XX KW keratinocyte; cervical cell; cervical tumour; ss.
XX XX
OS Synthetic.
OS Human papillomavirus 16.
XX WO9913071-A1.
XX PN
XX PD 18-MAR-1999.
XX PF 03-SEP-1998; 98WO-US18320.
XX PR 05-SEP-1997; 97US-0929140.
XX XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Alvarez-Salas L, Dipaolo J;
XX DR WPI: 1999-243727/20.
XX XX
PT New antisense oligonucleotide analogs for inhibiting growth of
PT cervical tumors
XX PS
XX PS Claim 6: Page 35; 40pp; English.
XX XX
CC This sequence represents an antisense oligonucleotide of the invention.
CC The antisense oligonucleotide analogs (ONS) have a sequence complementary
CC to a sequence of nucleotides 415-445 of human papilloma virus-16
CC (HPV-16). The antisense ONS can be used to inhibit expression of HPV gene
CC E6/E7 in living cells, preferably human keratinocytes or human cervical
CC cells. They bind to E6/E7 mRNA in the cell, prevent mRNA translation
CC and promote mRNA degradation by intracellular RNase H. They can be used
CC for preventing transformation of living cells by HPV. The antisense ONS
CC are used particularly for inhibiting the growth of cervical tumours.
XX SQ
Sequence 31 BP: 8 A; 5 C; 7 G; 11 U; 0 other:

Query Match      68.0%; Score 13.6; DB 20; Length 31;
Best Local Similarity 50.0%; Pred. No. 6.9e+02;
Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 1 ttcttcagtcacagctgt 20
   ::||| | ||| :
DB 1 uucucagagacagugcu 20

RESULT 10
AA075472
ID AA075472 standard; DNA; 49 BP.
XX
XX AC AA075472;
XX XX
XX DT 28-JUN-1995 (first entry)
XX XX
XX DE HPV primer probe HPV15.
XX XX
XX XX Human papilloma virus; HPV; HPV16; HPV18; diagnosis; primer; probe;
XX KW hybridization; self-sustained sequence replication; 3SR;
XX KW E6 protein; E7 protein; cervical dysplasia; cervix cancer; ss.
XX XX
XX OS Synthetic.
XX XX
XX PN WO9426934-A.
XX PD
XX PD 24-NOV-1994.
XX XX
XX PF 06-MAY-1994; 94WO-US05085.
XX PR
XX PR 06-MAY-1993; 93US-0058920.
XX PR

```

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XX PA (BAXT ) BAXTER DIAGNOSTICS INC.
XX XX
XX PI Brown JT;
XX XX
XX DR WPI: 1995-006821/01.
XX XX
XX PT human papilloma virus detection assay - by amplification using
XX PT self sustained sequence replication and hybridisation with a
XX PT detector probe
XX PS
XX PS Disclosure: Page 10; 79pp; English.
XX XX
XX CC Self-sustained sequence replication is performed on HPV E6/E7
XX CC region mRNA using 2 primers, one of which contains a
XX CC transcriptional promoter, pref. the primer T7 RNA-polymerase
XX CC binding site (AA075512). Suitable primers are given in AA075472-500.
XX CC Amplified sequences are hybridized to capture probes (AA075501-05),
XX CC and hybridization is detected using detection probes (AA075506-09,
XX CC AA086975). Expression of E6/E7 is diagnostic for cervical cancer
XX CC or pre-malignancy states.
XX SQ
Sequence 49 BP: 14 A; 10 C; 10 G; 15 T; 0 other:

Query Match      68.0%; Score 13.6; DB 16; Length 49;
Best Local Similarity 80.0%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ttcttcagtcacagctgt 20
   ||||| | ||| | |
DB 30 ttcttcagtcacagctgt 49

RESULT 11
AA068145/C
ID AA068145 standard; RNA; 27 BP.
XX
XX AC AA068145;
XX XX
XX DT 28-JUL-1999 (first entry)
XX XX
XX DE Human flt1 VEGF receptor hammethead ribozyme #871.
XX XX
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
XX KW flk-1; KDR; hammethead ribozyme; hairpin ribozyme; cleavage;
XX KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX KW foetal liver kinase 1; ss.
XX XX
XX OS Synthetic.
XX OS Homo sapiens.
XX XX
XX PN WO9715662-A2.
XX PD
XX PD 01-MAY-1997.
XX XX
XX PF 25-OCT-1996; 96WO-US17480.
XX XX
XX PR 11-JAN-1996; 96US-0584040.
XX PR 26-OCT-1995; 95US-0005974.
XX XX
XX PA (CHIR ) CHIRON CORP.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX XX
XX PI Escobedo J, McSwigen J, Pavco P, Stinchcomb D;
XX XX
XX DR WPI: 1997-259017/23.
XX XX
XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or
XX PT mRNA stability - useful for treating e.g. tumour angiogenesis,
XX PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX XX

```

PS Claim 9; Page 73; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (Flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.

SO Sequence 27 BP; 11 A; 4 C; 6 G; 5 U; 1 other:

Query Match 67.0%; Score 13.4; DB 18; Length 27;
Best Local Similarity 93.3%; Pred. No. 8.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 tcttcagtcacagc 16
11 |||||
DB 15 TCATCACTGCACACT 1

RESULT 12
AAV95515/c
ID AAV95515 standard; RNA; 27 BP.

XX AAV95515;
AC
DT 24-FEB-1999 (first entry)
XX
DE Human c-fos hammerhead ribozyme nucleotide position 1071.
XX
KM Human: c-fos: hammerhead ribozyme; hairpin ribozyme; target site;
KM cancer; oncogene; leukaemia; neuroblastoma; diagnosis; genetic drift;
KM mutation; diseased cell; ss.
XX
OS Synthetic.
OS Homo sapiens.
PN M09832846-A2.
XX
XX 30-JUL-1998.
XX
PF 20-JAN-1998; 98MO-US01017.
XX
XX 23-JAN-1997; 97US-0037658.
PR
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Jarvis T, MCSwigen JA, Stinchcomb DT;
XX WPI: 1998-427942/36.
DR
XX
XX Enzymatic nucleic acid molecules which specifically cleave RNA
PT derived from a c-fos gene - useful for treating conditions related
PT to levels of c-fos, especially cancer
XX
PS Claim 9; Page 51; 72pp; English.

XX The present invention describes an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from a c-fos gene. AAV95401 to AAV95540
CC and AAV95541 to AAV95584 represent hammerhead ribozymes and hairpin
CC ribozymes, respectively, which specifically cleave human c-fos. AAV95261
CC to AAV95500 and AAV95585 to AAV95628 represent human c-fos target
CC sequences. The enzymatic nucleic acid molecules can be used for treating
CC cancer associated with elevated levels of c-fos oncogene, especially
CC leukaemias, neuroblastomas and lung, breast and colon cancers. The
CC ribozymes may also be used as diagnostic tools to examine genetic drift
CC and mutations within diseased cells, or to detect the presence of c-fos
CC RNA in a cell.

XX Sequence 27 BP; 7 A; 7 C; 7 G; 5 U; 1 other:

SO

Query Match 67.0%; Score 13.4; DB 19; Length 27;
Best Local Similarity 93.3%; Pred. No. 8.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 tcttcagtcacagc 16
11 |||||
DB 15 TCATCACTGCACACT 1

RESULT 13
AAA88735
ID AAA88735 standard; DNA; 43 BP.

XX AAA88735;
AC
DT 05-FEB-2001 (first entry)
XX
DE Human FLINT mutagenic primer CF 110.
XX
DE FLINT: FAS ligand inhibitory protein; human; protease resistant;
KM acute lung injury; acute respiratory distress syndrome;
KM chronic obstructive pulmonary disease; pulmonary fibrosis;
KM ulcerative colitis; therapy; organ transplantation; mutagenesis;
KM PCR primer; strand overlap extension; ss.
XX
XX Homo sapiens.
PN M0200058466-A2.
XX
XX 05-OCT-2000.
XX
PF 20-MAR-2000; 2000MO-US06418.
XX
XX 30-MAR-1999; 99US-0126839.
PR 21-JUN-1999; 99US-0140073.
PR 04-AUG-1999; 99US-0147071.
PR 20-OCT-1999; 99US-0160524.
PR 21-OCT-1999; 99US-0160669.
PR 20-DEC-1999; 99US-0172744.
PR 26-JAN-2000; 2000US-0178184.
XX
XX (ELIL) LILLY & CO ELI.
XX
PI Micranovic R, Rathnachalam R, Witcher DR;
XX WPI: 2000-664925/64.
DR
XX
XX Novel protease resistant FAS ligand inhibitory protein analogues
PT resistant to in vivo or in vitro proteolysis at amino acid position 218
PT of the mature protein, useful for treating autoimmune diseases
XX
XX Example 1; Page 56; 100pp; English.

PS The present sequence is that of primer D (CF 110) used with
XX primers A (CF 107), B (CF 111) and C (CF 112) in a mutagenic PCR
CC process, involving a strand overlap extension (SOE) reaction, to
CC create a specific mutation in native FLINT cDNA (see AAA88730),
CC producing an R218Q mutant in which Arg-218 of native FLINT (see
CC AAB19705) is replaced by Gln (see AAB19709). The B and C primers are
CC targeted to the same area of the FLINT gene but on opposite
CC strands. Mismatch priming from both primers institutes the
CC mutation. The products are used as template for the A to D
CC reaction, which yields the desired mutated product. Claimed
CC analogues of FLINT, including the R218Q mutant, are resistant
CC to proteolytic cleavage, and are useful in the treatment of
CC acute lung injury, acute respiratory stress syndrome, ulcerative
CC colitis, chronic obstructive pulmonary disease, pulmonary
CC fibrosis, to inhibit T lymphocyte activation, and to facilitate
CC organ preservation for transplantation.

XX Sequence 43 BP: 13 A: 11 C: 14 G: 5 T: 0 other:
SQ

Query Match 67.0%; Score 13.4; DB 21; Length 43;
Best Local Similarity 93.3%; Pred. No. 9.3e+02;
Matches 14: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttctcagtcagcag 15
||| ||||| ||||| |||
Db 9 ttcatcagtcagcag 23

RESULT 14
AAD07384
ID AAD07384 standard; DNA: 43 BP.
XX AAD07384:
XX
DT 04-AUG-2001 (first entry)
XX
DE Mutagenic PCR primer D, CF110 to generate human FLINT variant, R218Q.
XX
XX Human: fas ligand inhibitory protein; FLINT; acute lung injury; ALI;
KM TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;
KM acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;
KM rheumatoid arthritis; fibroproliferative lung disease; acute lung injury; goitre;
KM fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;
KM chronic renal failure; graft-vs-host disease; cutaneous inflammation;
KM vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;
KM insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;
KM Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;
KM Down's syndrome; multiple sclerosis; cytostatic; neutropenic;
KM neuroprotective; vasoregic; mutagenic PCR primer; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX MO200142463-A1.
XX
PD 14-JUN-2001.
XX
XX 29-NOV-2000; 2000MO-US30166.
XX
XX 07-DEC-1999; 99US-0169367.
PR 07-DEC-1999; 99US-0169381.
PR 07-DEC-1999; 99US-0169412.
PR 23-MAR-2000; 2000US-0191430.
XX
XX (ELIL) LILLY & CO ELI.
XX
PI Lu J, Wilcher DR;
XX
XX WPI: 2001-381684/40.
XX
XX New FLINT polypeptide for treating and/or preventing acute lung injury,
PT acute respiratory distress syndrome, ulcerative colitis, and
PT graft-versus-host disease, comprises O-linked or N-linked
PT oligosaccharides -
XX
XX
XX Example 1: Page 32: 60pp: English.
XX
XX The present sequence is mutagenic reverse PCR primer D, CF110 which is
CC used to generate human mature fas ligand inhibitory protein (FLINT)
CC variant, R218Q. FLINT, a homologue of tumour necrosis factor receptor
CC protein (TNFR), binds fas ligand (FasL) and thereby preventing the
CC interaction of FasL with fas. FLINT comprising O-linked or N-linked
CC oligosaccharides is useful for preventing or treating acute lung injury
CC (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis, (PF),
CC chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),
CC to facilitate organ preservation for transplantation and to inhibit T
CC lymphocyte activation. FLINT is useful for treating and/or preventing

CC diseases such as rheumatoid arthritis, fibroproliferative lung disease,
CC fibrotic lung disease, acute lung injury, human immunodeficiency virus
CC (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-
CC host disease, cutaneous inflammation, vascular leak syndrome,
CC Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent
CC diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,
CC Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as
CC psoriasis, Down's syndrome, and multiple sclerosis.
XX
SQ Sequence 43 BP: 13 A: 11 C: 14 G: 5 T: 0 other:
XX

Query Match 67.0%; Score 13.4; DB 22; Length 43;
Best Local Similarity 93.3%; Pred. No. 9.3e+02;
Matches 14: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttctcagtcagcag 15
||| ||||| ||||| |||
Db 9 ttcatcagtcagcag 23

RESULT 15
AAZ67757
ID AAZ67757 standard; DNA: 47 BP.
XX
XX AAZ67757:
XX
DT 10-SEP-2001 (first entry)
XX
XX Human map-related biallelic marker SEQ ID NO: 2104.
DE
DE Human genome: biallelic marker; high density disequilibrium map;
KM genomic map; haplotype; phenotype; polymorphic base; genotyping;
KM haplotyping; hybridisation; identification; characterisation;
KM diagnosis; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
OS
XX
XX Key location/Qualifiers
FH variation replace(24,T)
FT /tag- a
FT /standard_name="single nucleotide polymorphism"
XX
XX MO954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99MO-1B00822.
XX
XX 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
XX (GENT) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI: 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
XX
XX Claim 1: Page 679; 2745pp: English.
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the

CC Characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 11 A; 11 C; 12 G; 13 T; 0 other;

Query Match 67.0%; Score 13.4; DB 21; Length 47;
Best Local Similarity 93.3%; Pred. No. 9.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ttcttcagtgccag 15
|||||||
Db 30 ttcttcagggccag 44

Search completed: December 26, 2001, 09:05:59
Job time: 721 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2001, 11:33:52 ; Search time 2376.51 Seconds
(without alignments)
138.835 Million cell updates/sec

Title: US-09-800-629a-62

Sequence: 1 ctggaagaagtcagatg 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 541028

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_ov:*
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8: gb_ov:*
9: gb_ov:*
10: gb_ov:*
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12: gb_ov:*
13: gb_ov:*
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15: gb_ov:*
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29: gb_ov:*
30: gb_ov:*
31: gb_ov:*
32: gb_ov:*
33: gb_ov:*
34: gb_ov:*
35: gb_ov:*
36: gb_ov:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	AR136259	AR136259 Sequence
2	20	100.0	33	I39778	I39778 Sequence 51
3	18.4	92.0	20	AR136259	AR136259 Sequence
4	15.2	76.0	20	AR136270	AR136270 Sequence
5	15	75.0	15	I39070	I39070 Sequence 10
6	14	70.0	15	I39071	I39071 Sequence 10
7	13.6	68.0	28	AR106113	AR106113 Sequence
8	12.8	64.0	50	AX157908	AX157908 Sequence
9	12.6	63.0	41	AR111652	AR111652 Sequence
10	12.6	63.0	41	AR147013	AR147013 Sequence
11	12.4	62.0	19	I17168	I17168 Sequence 23
12	12.4	62.0	21	DOC6P36A02	L27205 Dog Primer
13	12.4	62.0	30	AR090348	AR090348 Sequence
14	12.4	62.0	33	AR086954	AR086954 Sequence
15	12.4	62.0	33	AR095649	AR095649 Sequence
16	12.4	62.0	33	AR136117	AR136117 Sequence
17	12.4	62.0	36	AR099138	AR099138 Sequence
18	12	60.0	20	AR136271	AR136271 Sequence
19	12	60.0	26	AX044220	AX044220 Sequence
20	12	60.0	26	AX044225	AX044225 Sequence
21	12	60.0	26	AX044241	AX044241 Sequence
22	12	60.0	26	AX044246	AX044246 Sequence
23	12	60.0	26	AX044283	AX044283 Sequence
24	12	60.0	26	AX044288	AX044288 Sequence
25	11.8	59.0	20	AR136361	AR136361 Sequence
26	11.8	59.0	21	AX096200	AX096200 Sequence
27	11.8	59.0	25	AX166679	AX166679 Sequence
28	11.8	59.0	26	AR089887	AR089887 Sequence
29	11.8	59.0	30	AX060834	AX060834 Sequence
30	11.8	59.0	48	AX191999	AX191999 Sequence
31	11.8	59.0	50	I15482	I15482 Sequence 11
32	11.6	58.0	21	I13287	I13287 Sequence 19
33	11.6	58.0	25	AR001070	AR001070 Sequence
34	11.6	58.0	25	AR075397	AR075397 Sequence
35	11.6	58.0	25	AR142439	AR142439 Sequence
36	11.6	58.0	31	AR063482	AR063482 Sequence
37	11.6	58.0	31	AR063484	AR063484 Sequence
38	11.6	58.0	43	HS050443	HS050443 Human 180la
39	11.6	58.0	44	AR101938	AR101938 Sequence
40	11.6	58.0	45	BM0F185P	M10457 Bombyx mori
41	11.6	58.0	50	AX093077	AX093077 Sequence
42	11.4	57.0	39	A12211	A12211 FBI 660. 12
43	11.4	57.0	50	AX010685	AX010685 Sequence
44	11.2	56.0	20	A24703	A24703 Human tyros
45	11.2	56.0	20	AR119566	AR119566 Sequence

ALIGNMENTS

16-JUN-2001

PAT

LOCUS AR136259 20 bp DNA
DEFINITION Sequence 62 from patent US 6136603.
ACCESSION AR136259
VERSION AR136259.1 GI:14476931

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., Karras,J.G. and McKay,R.
TITLE Antisense modulation of interleukin-5 signal transduction
JOURNAL Patent: US 6136603-A 62 24-OCT-2000;
FEATURES Location/Qualifiers

BASE COUNT 5 a 3 c 6 g 6 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctggcaaatgtcagatg 20
|||||
Db 1 TCTGGCAAACTGTCTCAGTATG 20

RESULT 2

LOCUS 139778 33 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 51 from patent US 5616490.
ACCESSION 139778
VERSION 139778.1 GI:2084258
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 33)
AUTHORS Sullivan,S.M. and Draper,K.G.
TITLE Ribozymes targeted to TNF- α RNA
JOURNAL Patent: US 5616490-A 51 01-APR-1997;
FEATURES Location/Qualifiers
source 1..33

BASE COUNT 11 a 8 c 6 g 8 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctggcaaatgtcagatg 20
|||||
Db 28 TCTGGCAAACTGTCTCAGTATG 9

RESULT 3
LOCUS ARI36269 20 bp DNA PAT 16-JUN-2001
DEFINITION Sequence 72 from patent US 6136603.
ACCESSION ARI36269
VERSION ARI36269.1 GI:14476941
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., Karras,J.G. and McKay,R.
TITLE Antisense modulation of interleukin-5 signal transduction
JOURNAL Patent: US 6136603-A 72 24-OCT-2000;
FEATURES Location/Qualifiers
source 1..20

BASE COUNT 5 a 4 c 5 g 6 t
ORIGIN

Query Match 92.0%; Score 18.4; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctggcaaatgtcagatg 20
|||||
Db 1 TCTGGCAAACTGTCTCAGTATG 20

RESULT 4
LOCUS ARI36270 20 bp DNA PAT 16-JUN-2001

DEFINITION Sequence 73 from patent US 6136603.

ACCESSION ARI36270
VERSION ARI36270.1 GI:14476942

KEYWORDS
SOURCE Unknown.

ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., Karras,J.G. and McKay,R.
TITLE Antisense modulation of interleukin-5 signal transduction
JOURNAL Patent: US 6136603-A 73 24-OCT-2000;
FEATURES Location/Qualifiers
source 1..20

BASE COUNT 4 a 5 c 4 g 7 t
ORIGIN

Query Match 76.0%; Score 15.2; DB 6; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 tctggcaaatgtcagatg 20
|||||
Db 1 TCTGGCAAACTGTCTCAGTATG 20

RESULT 5
LOCUS 139070 15 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 108 from patent US 5616488.

ACCESSION 139070
VERSION 139070.1 GI:2083550
KEYWORDS
SOURCE Unknown.

ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE IL-5 targeted ribozymes
JOURNAL Patent: US 5616488-A 108 01-APR-1997;
FEATURES Location/Qualifiers
source 1..15

BASE COUNT 4 a 4 c 3 g 4 t
ORIGIN

Query Match 75.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctggcaaatgtca 15
|||||
Db 15 TCTGGCAAACTGTCA 1

RESULT 6
LOCUS 139071 15 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 109 from patent US 5616488.
ACCESSION 139071
VERSION 139071.1 GI:2083551
KEYWORDS
SOURCE Unknown.

ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE IL-5 targeted ribozymes
JOURNAL Patent: US 5616488-A 109 01-APR-1997;
FEATURES Location/Qualifiers
source 1..15

BASE COUNT 5 a 4 c 3 g 3 t
ORIGIN
Query Match 70.0%; Score 14; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tctgcaaatgtc 14
Db 14 TCTGGCAAGTGTCTC 1

RESULT 7
LOCUS AR106113 28 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6103514.
ACCESSION AR106113
VERSION AR106113.1 GI:12820178
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Natori, S.
TITLE Protease
JOURNAL Patent: US 6103514-A 9 15-AUG-2000;
FEATURES
source Location/Qualifiers
1..28
/organism="unknown"
BASE COUNT 10 a 8 c 5 g 5 t
ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 28;
Best Local Similarity 80.0%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 tctgcaaatgtcagatg 20
Db 23 TCTGGCACTGTCTGCATATG 4

RESULT 8
LOCUS AX157908 50 bp DNA PAT 22-JUN-2001
DEFINITION Sequence 1236 from Patent WO0140521.
ACCESSION AX157908
VERSION AX157908.1 GI:14539239
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 50)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE Shimketa, R.A. and Leach, M.
JOURNAL Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
Patent: WO 0140521-A 1236 07-JUN-2001;
FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number c928396311"
misc_feature 26
/note="2 of 2 allelic variants (1235 is other entry)"
BASE COUNT 10 a 12 c 19 g 9 t
ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 50;
Best Local Similarity 87.5%; Pred. No. 2.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 tctgcaaatgtcag 16
Db 25 TCCCGCAAGTGTCTCAG 10

RESULT 9
LOCUS AR11652 41 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 186 from patent US 6127163.
ACCESSION AR11652
VERSION AR11652.1 GI:12828500
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 41)
AUTHORS Cochran, M.D. and Junker, D.E.
TITLE Recombinant swinepox virus
JOURNAL Patent: US 6127163-A 186 03-OCT-2000;
FEATURES
source Location/Qualifiers
1..41
/organism="unknown"
BASE COUNT 17 a 5 c 6 g 13 t
ORIGIN

Query Match 63.0%; Score 12.6; DB 6; Length 41;
Best Local Similarity 78.9%; Pred. No. 3.8e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 tctgcaaatgtcagat 19
Db 8 TCTGGCATGTGTATATAT 26

RESULT 10
LOCUS AR147013 41 bp DNA PAT 08-AUG-2001
DEFINITION Sequence 74 from patent US 6221361.
ACCESSION AR147013
VERSION AR147013.1 GI:15110816
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 41)
AUTHORS Cochran, M.D. and Junker, D.E.
TITLE Recombinant swinepox virus
JOURNAL Patent: US 6221361-A 74 24-APR-2001;
FEATURES
source Location/Qualifiers
1..41
/organism="unknown"
BASE COUNT 17 a 5 c 6 g 13 t
ORIGIN

Query Match 63.0%; Score 12.6; DB 6; Length 41;
Best Local Similarity 78.9%; Pred. No. 3.8e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 tctgcaaatgtcagat 19
Db 8 TCTGGCATGTGTATATAT 26

RESULT 11
LOCUS 117168 19 bp DNA PAT 03-APR-1996
ORIGIN

```

DEFINITION Sequence 23 from patent US 5484886.
ACCESSION 117168
VERSION 117168.1 GI:1252076
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 19)
AUTHORS Fong,T.M. and Strader,C.D.
TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 5484886-A 23 16-JAN-1996;
FEATURES
  source
    1..19
    /organism="unknown"
BASE COUNT 5 a 7 c 1 g 6 t
ORIGIN

Query Match 62.0% Score 12.4; DB 6; Length 19;
Best Local Similarity 92.9%; Pred. NO. 4.9e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 aaagtgtcatgcatg 20
    ||| |||||
Db 18 AAAGGCTCAGTATG 5

RESULT 12
DOGP636A02
LOCUS DOGP636A02 21 bp DN
DEFINITION Dog primer for STS 636, 3' end. MAM 19-JAN-1996
ACCESSION L27205
VERSION L27205.1 GI:439191
KEYWORDS PCR identification; PCR primer; STS.
SEGMENT 2 of 2
SOURCE Canis familiaris (library: E. Ostrander, in pbluescript+) adult
  spleen DNA.
ORGANISM Canis familiaris
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
  1 (bases 1 to 21)
Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.
  One hundred and one new simple sequence repeat-based markers for
  the canine genome
  Mamm. Genome 6 (3), 192-195 (1995)
  95268214
COMMENT Submitted by:
  Fred Hutchinson Cancer Research Center
  Transplantation Biology Dept
  1124 Columbia; Mailstop M318
  Seattle, WA 98104, USA
  e-mail: eostrander@fhcrc.org
PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
PCR Profile: Denaturation: 94 degrees C for 1.00 minute
  Annealing: 55 or 59 degrees C for 0.45 minutes
  Polymerization: 74 degrees C for 1.00 minutes
  PCR Cycles: 33
  Final Extension: 74 degrees C for 5.00 minutes.
  Location/Qualifiers
    1..21
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    /db_xref="taxon:9615"
    /dev_stage="adult"
    /tissue_type="spleen"
    /tissue_lib="E. Ostrander, in pbluescript+"
    complement(1..21)
BASE COUNT 8 a 4 c 5 g 4 t
ORIGIN

Query Match 62.0% Score 12.4; DB 4; Length 21;
Best Local Similarity 92.9%; Pred. NO. 4.9e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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[illegible]

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Murphy,D., Reid,J. and Robertson,D.
TITLE Amidase
JOURNAL Patent: US 6004796-A 4 21-DEC-1999;
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"
BASE COUNT 13 a 8 c 7 g 5 t
ORIGIN

Query Match 62.0%; Score 12.4; DB 6; Length 33;
Best Local Similarity 92.9%; Pred. No. 4.9e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 ctggcaaaagtgtca 15
||||| |||||
DB 15 CTGGCACAGTGTCA 28

Search completed: December 21, 2001, 11:33:53
Job time: 16640 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2001, 08:38:29 : Search time 303.16 Seconds
(without alignments)
14,941 Million cell updates/sec

Title: US-09-800-629A-52
Perfect score: 20
Sequence: 1 tcttcagtcacagttgt 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 495388

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/2/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCRUS.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	US-09-280-799-52
2	20	100.0	24	1	US-08-592-126-14
3	20	100.0	24	2	US-08-687-080-14
4	14.4	72.0	24	1	US-08-200-807-3
5	14.4	72.0	24	1	US-08-488-305A-3
6	13.8	69.0	25	3	US-08-343-998-12
7	13.6	68.0	31	3	US-08-929-140-16
8	13.6	68.0	31	3	US-08-929-140-17
9	13.6	68.0	31	4	US-09-560-579A-16
10	13.6	68.0	31	4	US-09-560-579A-17
11	13.6	68.0	49	5	PCR-US94-05085A-3
12	13.6	68.0	49	5	PCR-US94-05085-3
13	13.4	67.0	27	3	US-08-998-099-255
14	13.2	66.0	34	2	US-08-606-288-1
15	13.2	66.0	34	3	US-09-347-483-1
16	13.2	66.0	50	5	PCR-US94-05085A-19
17	13.2	66.0	50	5	PCR-US94-05085-19
18	12.8	64.0	16	1	US-08-410-005-3
19	12.8	64.0	16	3	US-08-929-140-3
20	12.8	64.0	16	3	US-08-929-140-5
21	12.8	64.0	16	3	US-08-929-140-7
22	12.8	64.0	16	4	US-09-560-579A-3
23	12.8	64.0	16	4	US-09-560-579A-5
24	12.8	64.0	16	4	US-09-560-579A-7
25	12.8	64.0	17	1	US-08-410-005-4
26	12.8	64.0	20	4	US-09-042-353-341
27	12.8	64.0	20	4	US-09-487-445-104

28	12.8	64.0	20	4	US-08-758-417A-189	Sequence 189, App
29	12.8	64.0	50	5	PCR-US94-05085A-20	Sequence 20, Appl
30	12.8	64.0	50	5	PCR-US94-05085-20	Sequence 20, Appl
31	12.6	63.0	29	1	US-08-463-262A-17	Sequence 17, Appl
32	12.6	63.0	29	1	US-08-463-989-17	Sequence 17, Appl
33	12.6	63.0	29	4	US-09-003-574-17	Sequence 17, Appl
34	12.6	63.0	29	4	US-09-003-570-17	Sequence 17, Appl
35	12.6	63.0	29	4	US-08-584-760A-31	Sequence 31, Appl
36	12.6	63.0	31	1	US-08-524-757-34	Sequence 31, Appl
37	12.6	63.0	40	4	US-08-584-760A-32	Sequence 32, Appl
38	12.6	63.0	41	1	US-08-333-894-1	Sequence 32, Appl
39	12.4	62.0	25	4	US-08-638-931-22	Sequence 22, Appl
40	12.4	62.0	27	3	US-08-765-332-57	Sequence 57, Appl
41	12.2	61.0	20	4	US-09-487-445-30	Sequence 30, Appl
42	12.2	61.0	24	1	US-08-175-155-44	Sequence 44, Appl
43	12.2	61.0	24	1	US-08-477-509B-79	Sequence 79, Appl
44	12.2	61.0	24	2	US-08-707-237A-50	Sequence 50, Appl
45	12.2	61.0	24	3	US-08-482-085B-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
US-09-280-799-52
Sequence 52, Application US/09280799
Patent No. 6136603
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Kallay, James G.
APPLICANT: McKay, Robert
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
FILE REFERENCE: ISPH-0340
CURRENT APPLICATION NUMBER: US/09/280,799
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-280-799-52

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tcttcagtcacagttgt 20
Db 1 tcttcagtcacagttgt 20

RESULT 2
US-08-592-126-14/c
Sequence 14, Application US/08592126
Patent No. 5821091
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESS: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,126
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Primer IL5-1
; US-08-592-126-14

Query Match          100.0%; Score 20; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ttcttcagtcacagttgct 20
Db 21 ttcttcagtcacagttgct 2

RESULT 3
US-08-687-080-14/c
; Sequence 14, Application US/08687080
; Patent No. 5965427
; GENERAL INFORMATION:
; APPLICANT: Gregory Dolganov
; TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,080
; FILING DATE: 17-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,126
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 14:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Primer IL5-1
; US-08-687-080-14

Query Match          100.0%; Score 20; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ttcttcagtcacagttgct 20
Db 21 ttcttcagtcacagttgct 2

RESULT 4
US-08-200-807-3/c
; Sequence 3, Application US/08200807
; Patent No. 5573939
; GENERAL INFORMATION:
; APPLICANT: B vix, Claes Olof, Eriksson, Ulf
; TITLE OF INVENTION: Isolated Protein Receptors, Antibodies Which
; TITLE OF INVENTION: bind Thereto, Nucleic Acid Sequence Coding
; Patent No. 5573939
; TITLE OF INVENTION: Theretof, And Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felle & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,807
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/883,539
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5573939man D.
; REGISTRATION NUMBER: 30,946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; US-08-200-807-3

Query Match          72.0%; Score 14.4; DB 1; Length 24;
Best Local Similarity 93.8%; Pred. No. 77;
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 tcaatgcacagtttgt 20

DB 18 TCAGTCACAGTTGT 3

RESULT 5

US-08-488-305A-3/C

Sequence 3, Application US/08488305A

Patent No. 5679772

GENERAL INFORMATION:

APPLICANT: B vik, Claes Olaf; Eriksson, Ulf; Peterson, Per A.

TITLE OF INVENTION: Isolated Protein Receptors, Antibodies which

TITLE OF INVENTION: bind Thereeto, Nucleic Acid Sequence Coding

Patent No. 5679772

TITLE OF INVENTION: Therefore, And Uses Thereof

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felte & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 Inch, 1.44 Kb storage

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,305A

FILING DATE: 7-JUNE-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Kohl, Vineet

REGISTRATION NUMBER: 37,003

REFERENCE/DOCKET NUMBER: LUD 5280.3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 688-9200

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: no

ANTI-SENSE: no

US-08-488-305A-3

Query Match 72.0%; Score 14.4; DB 1; Length 24;

Best Local Similarity 93.8%; Pred. No. 77;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 tcaatgcacagtttgt 20

DB 18 TCAGTCACAGTTGT 3

RESULT 6

US-08-343-998-12/C

Sequence 12, Application US/08343998A

Patent No. 6020123

GENERAL INFORMATION:

APPLICANT: Sonigo, Pierre

APPLICANT: Brechot, Christian

APPLICANT: Courgard, Valerie

TITLE OF INVENTION: OLIGONUCLEOTIDE SEQUENCES FOR THE AMPLIFICATION OF THE

TITLE OF INVENTION: GENOME OF THE RETROVIRUSES OF THE HIV-2 AND SIV TYPE,

TITLE OF INVENTION: AND THEIR USES FOR IN VITRO DIAGNOSIS OF THE INFECTIONS

TITLE OF INVENTION: DUE TO THESE VIRUSES

FILE REFERENCE: 2356.0065-01

CURRENT APPLICATION NUMBER: US/08/343,998A

CURRENT FILING DATE: 1994-11-18

EARLIER APPLICATION NUMBER: 07/820,600

EARLIER FILING DATE: 1992-01-22

EARLIER APPLICATION NUMBER: PCT/FR90/00394

EARLIER FILING DATE: 1990-06-05

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO: 12

LENGTH: 25

TYPE: DNA

ORGANISM: Human immunodeficiency virus type 2

FEATURE:

US-08-343-998-12

Query Match 69.0%; Score 13.8; DB 3; Length 25;

Best Local Similarity 88.2%; Pred. No. 1.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 ctcaatgcacagtttg 19

DB 24 CTTAGTCACAGTCG 8

RESULT 7

US-08-929-140-16

Sequence 16, Application US/08929140

Patent No. 6084090

GENERAL INFORMATION:

APPLICANT: DiPaolo, Joseph

APPLICANT: Alvarez-Salas, Luis

TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS INHIBITION

TITLE OF INVENTION: BY ANTISENSE OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear

STREET: 620 Newport Center Drive

CITY: Newport Beach

STATE: CA

COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/929,140

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: NIH138.001A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 714/760-0404

TELEFAX: 714/760-9503

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-929-140-16

Alvarez-Salas, Luis

SOFTWARE: FastSEO for Win

SOFTWARE: FastSEO for Win

SOFTWARE: FastSEO for Win

```

: APPLICATION NUMBER: US/09/560,579A
: FILING DATE: 28-Apr-2000
: CLASSIFICATION: <Unknown>
: PRIORITY NUMBER: 08/929,140
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Altman, Daniel E
: REGISTRATION NUMBER: 34,115
: REFERENCE/DOCKET NUMBER: NIH138,001A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 714/760-0404
: TELEFAX: 714/760-9503
: TELEX: <Unknown>
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 31 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: SEQUENCE DESCRIPTION: SEQ ID NO: 17:
: US-09-560-579A-17
:
: Query Match      68.0% Score 13.6; DB 4; Length 31:
: Best Local Similarity 80.0%; Pred. No. 2e+02:
: Matches 16: Conservative 0; Mismatches 4; Indels 0; Gaps 0:
:
: Oy      1 ttcttcagtcacagttggt 20
:         ||||| ||||| ||
: Db      1 ttcttcagtcacagtcgct 20
:
: RESULT 11
: PCT-US94-05085A-3
: Sequence 3, Application PC/TUS9405085A
: GENERAL INFORMATION:
: APPLICANT: Janice T. Brown
: TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS DETECTION ASSAY
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Baxter Diagnostics Inc.
: STREET: One Baxter Parkway, Building DP-3E
: CITY: Deerfield
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60015
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: Apple Macintosh System 7.0
: SOFTWARE: Macintosh Text File
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/05085A
: FILING DATE: N/A
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/058,920
: FILING DATE: May 6, 1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Mark Buonaiuto
: REGISTRATION NUMBER: 31,593
: REFERENCE/DOCKET NUMBER: BA-4448
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 708/948-2537
: TELEFAX: 708/948-2642
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 49
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE:
: DESCRIPTION: Other nucleic acid, synthetic DNA
: HYPOTHETICAL: no
: ANTI-SENSE: no
: IMMEDIATE SOURCE:
: LIBRARY: DNA synthesizer
: FEATURE:
: NAME/KEY: HPV15. Phage T7 RNA polymerase binding site at 5'end, followed by
: PCT-US94-05085A-3
:
: Query Match      68.0% Score 13.6; DB 5; Length 49:
: Best Local Similarity 80.0%; Pred. No. 2.1e+02:
: Matches 16: Conservative 0; Mismatches 4; Indels 0; Gaps 0:
:
: Oy      1 ttcttcagtcacagttggt 20
:         ||||| ||||| ||
: Db      30 ttcttcagtcacacagtcgct 49
:
: RESULT 12
: PCT-US94-05085-3
: Sequence 3, Application PC/TUS9405085
: GENERAL INFORMATION:
: APPLICANT: Janice T. Brown
: TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS DETECTION ASSAY
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Baxter Diagnostics Inc.
: STREET: One Baxter Parkway, Building DP-3E
: CITY: Deerfield
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60015
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: Apple Macintosh
: SOFTWARE: Macintosh Text File
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/05085
: FILING DATE: 06-MAY-1994
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/058,920
: FILING DATE: May 6, 1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Mark Buonaiuto
: REGISTRATION NUMBER: 31,593
: REFERENCE/DOCKET NUMBER: BA-4448
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 708/948-2537
: TELEFAX: 708/948-2642
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 49
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE:
: DESCRIPTION: Other nucleic acid, synthetic DNA
: HYPOTHETICAL: no
: ANTI-SENSE: no
: IMMEDIATE SOURCE:
: LIBRARY: DNA synthesizer
: FEATURE:
: NAME/KEY: HPV15. Phage T7 RNA polymerase binding site at 5'end, followed by
: PCT-US94-05085-3
:
: Query Match      68.0% Score 13.6; DB 5; Length 49:
: Best Local Similarity 80.0%; Pred. No. 2.1e+02:
: Matches 16: Conservative 0; Mismatches 4; Indels 0; Gaps 0:
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OY 1 tcttcagtgacagctggt 20
||||| |||||
Db 30 TTCCTGAGACAGTGGCT 49

RESULT 13

US-08-998-099-255/c
; Sequence 255, Application US/08998099A
; Patent No. 6103890
; GENERAL INFORMATION:
; APPLICANT: JARVIS, THALE
; APPLICANT: MCSWIGEN, JAMES A.
; APPLICANT: STINCHCOMB, DAN T.
; TITLE OF INVENTION: ENZYMAIC ACID TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
; FILE REFERENCE: 231/175
; CURRENT APPLICATION NUMBER: US/08/998,099A
; EARLIER FILING DATE: 1997-12-24
; EARLIER APPLICATION NUMBER: 60/037,658
; EARLIER FILING DATE: 1997-01-23
; EARLIER APPLICATION NUMBER: 08/373,124
; EARLIER FILING DATE: 1995-01-13
; EARLIER APPLICATION NUMBER: 08/245,466
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 255
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized Hammerhead Ribozyme
US-08-998-099-255

Query Match

Best Local Similarity 93.3%; Score 13.4; DB 3; Length 27;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 tcttcagtgacagct 16
|| |||||
Db 15 TCATCAGTGCACACT 1

RESULT 14

US-08-606-288-1
; Sequence 1, Application US/08606288
; Patent No. 5955087
; GENERAL INFORMATION:
; APPLICANT: Whittle, N.R.
; APPLICANT: Carmichael, J.P.
; APPLICANT: Connor, S.E.
; APPLICANT: Thompson, H.S.G.
; APPLICANT: Wilson, M.J.
; TITLE OF INVENTION: Polypeptides useful as immunotherapeutic
; TITLE OF INVENTION: Agents, and Methods of Polypeptide Preparation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Suite 3400, Four Embarcadero Center
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,288

FILING DATE: 23-FEB-1996

PRIOR APPLICATION DATA: GB 9503786.7

FILING DATE: 24-FEB-1995

PRIOR APPLICATION DATA: US 60/000034

FILING DATE: 08-JUN-1995

PRIOR APPLICATION DATA: GB 9515478.7

FILING DATE: 28-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Walter H. Dreger

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-63284/WHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 34 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

HYPOTHETICAL: NO

AMTI-SENSE: NO

US-08-606-288-1

Query Match

Best Local Similarity 66.0%; Score 13.2; DB 2; Length 34;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 tcttcagtgacagctg 19
||||| |||||
Db 13 TTCCTGAGTGCAGTGG 30

RESULT 15

US-09-347-483-1
; Sequence 1, Application US/09347483
; Patent No. 6123948
; GENERAL INFORMATION:
; APPLICANT: Whittle, N.R.
; APPLICANT: Carmichael, J.P.
; APPLICANT: Connor, S.E.
; APPLICANT: Thompson, H.S.G.
; APPLICANT: Wilson, M.J.
; TITLE OF INVENTION: Polypeptides useful as immunotherapeutic
; TITLE OF INVENTION: Agents, and Methods of Polypeptide Preparation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Suite 3400, Four Embarcadero Center
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/347,483
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/606,288
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000034
; FILING DATE: 08-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9515478.7
; FILING DATE: 28-JUL-1995

ATTORNEY/AGENT INFORMATION:
NAME: Walter H. Dreger
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63284/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-347-483-1

Query Match 66.0%; Score 13.2; DB 3; Length 34;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2 tcttcagtgacacgltgg 19
||||| ||||| ||| |||
Db 13 TCTTCGCTGCCGACATCG 30

Search completed: December 21, 2001, 11:39:04
Job time: 10835 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2001, 11:39:05 : Search time 303.16 Seconds
(without alignments)
14.941 Million cell updates/sec

Title: US-09-800-629a-62

Sequence: 1 tctggcaagtgctcagatg 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 495388

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: /cgn2_6/ptodata/2/lna/5A.COMB.seq.*
2: /cgn2_6/ptodata/2/lna/5B.COMB.seq.*
3: /cgn2_6/ptodata/2/lna/6A.COMB.seq.*
4: /cgn2_6/ptodata/2/lna/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/lna/PCITUS.COMB.seq.*
6: /cgn2_6/ptodata/2/lna/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	US-09-280-799-62
2	20	100.0	33	1	US-08-434-503-51
3	18.4	92.0	20	3	US-09-280-799-72
4	15.2	76.0	20	3	US-09-280-799-73
5	13	75.0	15	1	US-08-319-928-108
6	14	70.0	15	1	US-08-319-928-109
7	13.6	68.0	28	3	US-09-120-365-9
8	13.6	68.0	28	4	US-09-515-039-9
9	12.6	63.0	41	3	US-08-480-640A-186
10	12.6	63.0	41	3	US-08-295-802-186
11	12.6	63.0	41	4	US-08-686-968C-74
12	12.6	63.0	41	4	US-08-488-237A-186
13	12.4	62.0	19	1	US-08-117-965-53
14	12.4	62.0	30	2	US-08-859-998-468
15	12.4	62.0	33	2	US-08-664-646A-4
16	12.4	62.0	33	2	US-09-066-385-4
17	12.4	62.0	33	3	US-09-261-006-4
18	12.4	62.0	33	3	US-08-951-088-4
19	12.4	62.0	36	3	US-09-023-082A-3
20	12.2	61.0	18	3	US-09-344-520-39
21	12.2	61.0	21	6	5455029-28
22	12	60.0	20	3	US-09-280-799-74
23	12	60.0	35	4	US-09-428-292-9
24	11.8	59.0	20	3	US-09-280-799-164
25	11.8	59.0	26	1	US-08-859-998-7
26	11.8	59.0	56	2	US-08-178-606-11
27	11.6	58.0	21	1	US-08-222-177A-199

28	11.6	58.0	21	4	US-09-019-160-79	Sequence 79, App1
C 29	11.6	58.0	25	1	US-08-438-753B-14	Sequence 14, App1
C 30	11.6	58.0	25	1	US-08-443-883A-14	Sequence 14, App1
C 31	11.6	58.0	25	2	US-08-631-328-14	Sequence 14, App1
C 32	11.6	58.0	25	2	US-08-455-524B-14	Sequence 14, App1
C 33	11.6	58.0	25	2	US-08-455-021B-14	Sequence 14, App1
C 34	11.6	58.0	25	4	US-09-045-467-14	Sequence 14, App1
C 35	11.6	58.0	31	2	US-08-077-251-6	Sequence 6, App1
C 36	11.6	58.0	31	2	US-08-077-251-6	Sequence 6, App1
C 37	11.6	58.0	44	3	US-08-989-251-11	Sequence 11, App1
C 38	11.6	58.0	44	3	US-09-340-250-11	Sequence 11, App1
C 39	11.4	57.0	18	4	US-08-478-316-94	Sequence 94, App1
C 40	11.4	57.0	19	4	US-09-338-907-537	Sequence 537, App
C 41	11.4	57.0	24	2	US-08-360-606B-26	Sequence 26, App1
C 42	11.4	57.0	30	4	US-09-230-199-24	Sequence 24, App1
C 43	11.4	57.0	47	4	US-09-338-907-220	Sequence 220, App
C 44	11.4	57.0	47	4	US-09-338-907-297	Sequence 297, App
C 45	11.2	56.0	20	3	US-08-987-326-7	Sequence 7, App1

ALIGNMENTS

RESULT 1
US-09-280-799-62
Sequence 62, Application US/09280799
Patent No. 6136603
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Karris, James G.
APPLICANT: McKay, Robert
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
FILE REFERENCE: ISPH-0340
CURRENT APPLICATION NUMBER: US/09/280,799
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 62
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-280-799-62

Query Match 100.0%; Score 20; DB 3; Length 20;

Best Local Similarity 100.0%; Pred No. 0.029; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 tctggcaagtgctcagatg 20
1 tctggcaagtgctcagatg 20

RESULT 2
US-08-434-503-51/C
Sequence 51, Application US/08434503
Patent No. 5616490
GENERAL INFORMATION:
APPLICANT: Sean M. Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: TREATMENT OF INFLAMMATORY
DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA

ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,503
FILING DATE: 04-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,895
FILING DATE: 19-JAN-1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 200/276
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 33
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-434-503-51

Query Match 100.0%; Score 20; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctggcaagtcagtcagt 20
|||||
DB 28 tctggcaagtcagtcagt 9

RESULT 3
US-09-280-799-72
Sequence 72, Application US/09280799
Patent No. 6136603
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Karras, James G.
APPLICANT: McKay, Robert
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
FILE REFERENCE: ISPH-0340
CURRENT APPLICATION NUMBER: US/09/280,799
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 72
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-280-799-72

Query Match 92.0%; Score 18.4; DB 3; Length 20;
Best Local Similarity 95.0%; Pred. No. 0.21;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctggcaagtcagtcagt 20
|||||
DB 1 tctggcaagtcagtcagt 20

RESULT 4
US-09-280-799-73
Sequence 73, Application US/09280799
Patent No. 6136603
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Karras, James G.
APPLICANT: McKay, Robert
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
FILE REFERENCE: ISPH-0340
CURRENT APPLICATION NUMBER: US/09/280,799
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 73
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-280-799-73

Query Match 76.0%; Score 15.2; DB 3; Length 20;
Best Local Similarity 85.0%; Pred. No. 11;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 tctggcaagtcagtcagt 20
|||||
DB 1 tctggcaagtcagtcagt 20

RESULT 5
US-08-319-492B-108/c
Sequence 108, Application US/08319492B
Patent No. 5616488
GENERAL INFORMATION:
APPLICANT: Sullivan, Sean M.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwigen, James
APPLICANT: Slinchcomb, Dan T.
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
NUMBER OF SEQUENCES: 751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,492B
FILING DATE: October 7, 1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard

Two

REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/276
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-319-492B-108

Query Match 75.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctggcaagtgatca 15
|||||
DB 15 TCTGCCAAGTGTCA 1

RESULT 6

US-08-319-492B-109/C
Sequence 109, Application US/08319492B
Patent No. 5616488

GENERAL INFORMATION:
APPLICANT: Sullivan, Sean M.
APPLICANT: Draper, Kenneth G.
APPLICANT: MCSwigen, James
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF IL-5
NUMBER OF SEQUENCES: 751
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/319,492B
FILING DATE: October 7, 1994

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008, 895
FILING DATE: January 19, 1993

Two

APPLICATION NUMBER: 07/989, 849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/276
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 109:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
US-08-319-492B-109

Query Match 70.0%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctggcaagtgatc 14
|||||
DB 14 TCTGCCAAGTGTCA 1

RESULT 7

US-09-120-365-9/C
Sequence 9, Application US/09120365
Patent No. 6103514

GENERAL INFORMATION:

APPLICANT: Natori, Shunji
TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
CURRENT APPLICATION NUMBER: US/09/120,365
CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: JP 9-333 474
EARLIER FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9

LENGTH: 28

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURES: OTHER INFORMATION: Description of Artificial Sequence: primer

US-09-120-365-9

Query Match 68.0%; Score 13.6; DB 3; Length 28;
Best Local Similarity 80.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 tctggcaagtgatcatg 20
|||||
DB 23 TCTGCCACTGTCCATATG 4

RESULT 8

US-09-515-039-9/C
Sequence 9, Application US/09515039
Patent No. 6214599

GENERAL INFORMATION:

APPLICANT: Natori, Shunji
TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
CURRENT APPLICATION NUMBER: US/09/515,039
CURRENT FILING DATE: 2000-03-06
EARLIER APPLICATION NUMBER: JP 9-333 474
EARLIER FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9

LENGTH: 28

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURES:

OTHER INFORMATION: Description of Artificial Sequence: primer

US-09-515-039-9

Query Match 68.0%; Score 13.6; DB 4; Length 28;
Best Local Similarity 80.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;


```

; APPLICANT: Junker, David E.
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,237A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-488-237A-186

Query Match      63.0%; Score 12.6; DB 4; Length 41;
Best Local Similarity 78.9%; Pred. No. 3.2e+02;
Matches 15: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tctggcaaaagtgcagat 19
   ||||| ||||| |||
Db 8 TCTGCATGTGTATTAT 26

RESULT 13
; US-08-117-965-23/c
; Sequence 23, Application US/08117965
; Patent No. 5484886
; GENERAL INFORMATION:
; APPLICANT: Tung, Fong M.
; TITLE OF INVENTION: Human Neurokinin-1 Receptor
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,965
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 691,197
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```

; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Nicholson, William H.
; REGISTRATION NUMBER: 25,147
; REFERENCE/DOCKET NUMBER: 18387
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5315
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; US-08-117-965-23

Query Match      62.0%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 3.5e+02;
Matches 13: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 aaagtcagatcg 20
   ||| ||||| |||
Db 18 AAAGGTCAGATG 5

RESULT 14
; US-08-859-998-468
; Sequence 468, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-0875
; TELEFAX: 415-322-5070
; INFORMATION FOR SEQ ID NO: 468:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
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US-08-859-998-468

Query Match 62.0%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 3.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 tggcaagtlcag 16
|||||
DB 15 TGCACAGTGTGAG 28

RESULT 15
US-08-664-646A-4
; Sequence 4, Application US/08664646A
; Patent No. 5877001

GENERAL INFORMATION:

APPLICANT: Murphy et al.
TITLE OF INVENTION: Amldases
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/664,646A
FILING DATE: June 17, 1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Charles J. Herron
REGISTRATION NUMBER: 28,019

REFERENCE/DOCKET NUMBER: 331400-53
TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 NUCLEOTIDES
TYPE: NUCLEIC ACID

STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR

MOLECULE TYPE: Oligonucleotide
US-08-664-646A-4

Query Match 62.0%; Score 12.4; DB 2; Length 33;
Best Local Similarity 92.9%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ctggcaagtlcag 15
|||||
DB 15 CTGCACAGTGTGCA 28

Search completed: December 21, 2001, 11:39:06
Job time: 10837 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2001, 11:34:01 ; Search time 2376.51 Seconds
(without alignments)
104.127 Million cell updates/sec

Title: US-09-800-629A-209

Perfect score: 15

Sequence: 1 Lctaccaagacttc 15

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1472140 segs, 8248589755 residues 541028

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
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8: gb_pl:*
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12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: gb_vl:*
16: em_da:*
17: em_fun:*
18: em_hum:*
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21: em_or:*
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25: em_ro:*
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27: em_sy:*
28: em_un:*
29: em_vl:*
30: em_htgo_hum:*
31: em_htgo_inv:*
32: em_htgo_rtd:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rtd:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15	100.0	20	6	AR136332	AR136332 Sequence
2	15	100.0	20	6	AR144274	AR144274 Sequence
3	13.4	89.3	20	6	AR136346	AR136346 Sequence
4	13.4	89.3	20	6	AR144285	AR144285 Sequence
5	13.4	89.3	20	6	AR144300	AR144300 Sequence
6	12	80.0	27	6	AX118436	AX118436 Sequence
7	11.8	78.7	28	6	AR090369	AR090369 Sequence
8	11.8	78.7	34	6	AR085821	AR085821 Sequence
9	11.8	78.7	37	6	AR000592	AR000592 Sequence
10	11.8	78.7	37	6	AR000593	AR000593 Sequence
11	11.8	78.7	48	6	AR085815	AR085815 Sequence
12	11.8	78.7	48	6	AR091644	AR091644 Sequence
13	11.4	76.0	21	6	AR058934	AR058934 Sequence
14	11.4	76.0	21	6	168720	168720 Sequence 22
15	11.4	76.0	24	6	AR019297	AR019297 Sequence
16	11.4	76.0	24	6	AR061841	AR061841 Sequence
17	11.4	76.0	24	6	AR079365	AR079365 Sequence
18	11.4	76.0	24	6	AR147552	AR147552 Sequence
19	11.4	76.0	24	6	134711	134711 Sequence 3
20	11.4	76.0	24	6	167965	167965 Sequence 3
21	11.4	76.0	39	6	AX080330	AX080330 Sequence
22	11	73.3	22	6	AR106133	AR106133 Sequence
23	10.8	72.0	18	6	AI6427	AI6427 synthetic o
24	10.8	72.0	20	6	AR136347	AR136347 Sequence
25	10.8	72.0	20	6	AR144286	AR144286 Sequence
26	10.8	72.0	20	6	AR144301	AR144301 Sequence
27	10.8	72.0	21	6	AR148681	AR148681 Sequence
28	10.8	72.0	22	6	AR085274	AR085274 Sequence
29	10.8	72.0	22	6	AR085275	AR085275 Sequence
30	10.8	72.0	22	6	117705	117705 Sequence 4
31	10.8	72.0	22	6	117706	117706 Sequence 5
32	10.8	72.0	22	6	138617	138617 Sequence 4
33	10.8	72.0	22	6	138618	138618 Sequence 5
34	10.8	72.0	23	6	169338	169338 Sequence 10
35	10.8	72.0	23	6	AR106295	AR106295 Sequence
36	10.8	72.0	25	6	AX042926	AX042926 Sequence
37	10.8	72.0	25	6	E13467	E13467 PCR primer
38	10.8	72.0	25	9	HUMXPC6A10A	L32075 Homo sapien
39	10.8	72.0	27	6	AX012391	AX012391 Sequence
40	10.8	72.0	27	6	E59997	E59997 Highly acti
41	10.8	72.0	29	6	AX09585	AX09585 Sequence
42	10.8	72.0	31	6	137195	137195 Sequence 20
43	10.8	72.0	31	6	137196	137196 Sequence 20
44	10.8	72.0	31	6	137197	137197 Sequence 21
45	10.8	72.0	31	6	137198	137198 Sequence 21

ALIGNMENTS

RESULT 1
AR136332
LOCUS AR136332 20 bp DNA
DEFINITION Sequence 135 from patent US 6136603.
ACCESSION AR136332
VERSION AR136332.1 GI:14477004
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., Karras,J.G. and McKay,R.
TITLE Antisense modulation of interleukin-5 signal transduction
JOURNAL Patent: US 6136603-A 135 24-OCT-2000;
FEATURES
source Location/Qualifiers
BASE COUNT 5 a 7 c 3 g 5 t
ORIGIN

Patent

Query Match 100.0%; Score 15; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctaccaaggacttc 15
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DB 6 TCTATCAGGACTTC 20

RESULT 2
LOCUS AR144274 20 bp DNA PAT 08-AUG-2001
DEFINITION Sequence 2 from patent US 6210892.
ACCESSION AR144274
VERSION AR144274.1 GI:15106141
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank, Cooke,S.T., Manoharan,M., Wyatt,J.R., Baker,B.F.,
Monta,B.P., Freier,S.M., McKay,R. and Karras,J.G.
TITLE Alteration of cellular behavior by antisense modulation of mRNA
PROCESSING
JOURNAL Patent: US 6210892-A 2 03-APR-2001;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT 5 a 7 c 3 g 5 t
ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctaccaaggacttc 15
|||||
DB 6 TCTATCAGGACTTC 20

Interfered

RESULT 3
LOCUS AR136346 20 bp DNA PAT 16-JUN-2001
DEFINITION Sequence 149 from patent US 6136603.
ACCESSION AR136346
VERSION AR136346.1 GI:14477018
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., Karras,J.G. and McKay,R.
TITLE Antisense modulation of interleukin-5 signal transduction
JOURNAL Patent: US 6136603-A 149 24-OCT-2000;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT 5 a 6 c 3 g 6 t
ORIGIN

Query Match 89.3%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctaccaaggacttc 15
|||||
DB 6 TCTATCAGGACTTC 20

RESULT 4

AR144285
LOCUS AR144285 20 bp DNA PAT 08-AUG-2001
DEFINITION Sequence 13 from patent US 6210892.
ACCESSION AR144285
VERSION AR144285.1 GI:15106152
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank, Cooke,S.T., Manoharan,M., Wyatt,J.R., Baker,B.F.,
Monta,B.P., Freier,S.M., McKay,R. and Karras,J.G.
TITLE Alteration of cellular behavior by antisense modulation of mRNA
PROCESSING
JOURNAL Patent: US 6210892-A 13 03-APR-2001;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT 5 a 6 c 3 g 6 t
ORIGIN

Query Match 89.3%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctaccaaggacttc 15
|||||
DB 6 TCTATCAGGACTTC 20

RESULT 5
LOCUS AR144300 20 bp DNA PAT 08-AUG-2001
DEFINITION Sequence 28 from patent US 6210892.
ACCESSION AR144300
VERSION AR144300.1 GI:15106167
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank, Cooke,S.T., Manoharan,M., Wyatt,J.R., Baker,B.F.,
Monta,B.P., Freier,S.M., McKay,R. and Karras,J.G.
TITLE Alteration of cellular behavior by antisense modulation of mRNA
PROCESSING
JOURNAL Patent: US 6210892-A 28 03-APR-2001;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT 5 a 6 c 3 g 6 t
ORIGIN

Query Match 89.3%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctaccaaggacttc 15
|||||
DB 6 TCTATCAGGACTTC 20

RESULT 6
LOCUS AX118436 27 bp DNA PAT 11-MAY-2001
DEFINITION Sequence 3559 from Patent WO0129262.
ACCESSION AX118436
VERSION AX118436.1 GI:14035387
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequence.

REFERENCE 1 (bases 1 to 27)
 AUTHORS Picoult-Newburg, L. and Pohl, M.
 TITLE Genotyping reagents, kits and methods of use thereof
 JOURNAL Patent: WO 0129262-A 3559 26-APR-2001;
 Orchid Biosciences, Inc. (US)
 FEATURES
 source Location/Qualifiers
 1..27
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Primer"
 misc_feature 1..27
 /note="n = C3 linker"
 BASE COUNT 5 a 5 c 7 g 9 t 1 others
 ORIGIN

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 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ctaccaagact 13
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 Db 15 CTACCAAGACT 4

RESULT 7
 LOCUS AR090369 28 bp DNA PAT 07-SEP-2000
 DEFINITION Sequence 489 from patent US 5994076.
 ACCESSION AR090369
 VERSION AR090369.1 GI:10017124
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 28)
 AUTHORS Chenchik, A., Jekhadze, G. and Bishlavskii, R.
 TITLE Methods of assaying differential expression
 JOURNAL Patent: US 5994076-A 489 30-NOV-1999;
 FEATURES
 source Location/Qualifiers
 1..28
 /organism="unknown"
 BASE COUNT 5 a 5 c 8 g 10 t
 ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 28;
 Best Local Similarity 86.7%; Pred. No. 3.1e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaagactc 15
 |||||
 Db 21 TCTACCAAGACTC 7

RESULT 8
 LOCUS AR085821 34 bp DNA PAT 07-SEP-2000
 DEFINITION Sequence 16 from patent US 5985281.
 ACCESSION AR085821
 VERSION AR085821.1 GI:10012587
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)
 AUTHORS Taylorson, C. John, Eggelte, H. Johannes, Taragona-Fiol, A.,
 Rabin, B. Robert, Boyle, F. Thomas, Hennam, J. Frederick,
 Blakey, D. Charles, Marsham, P. Robert, Heaton, D. William, Davies, D. Huw,
 Slater, A. Michael and Hennequin, L. FrancoisAndre.
 TITLE Chemical compounds
 JOURNAL Patent: US 5985281-A 16 16-NOV-1999;
 FEATURES Location/Qualifiers

source 1..34
 /organism="unknown"
 BASE COUNT 10 a 6 c 9 g 9 t
 ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 34;
 Best Local Similarity 86.7%; Pred. No. 3e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaagactc 15
 |||||
 Db 19 TCTACCAAGACTC 5

RESULT 9
 LOCUS AR000592 37 bp DNA PAT 04-DEC-1998
 DEFINITION Sequence 24 from patent US 5736524.
 ACCESSION AR000592
 VERSION AR000592.1 GI:3963123
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 37)
 AUTHORS Content, J., Huygen, K., Liu, M. A., Montgomery, D. and Uimer, J.
 TITLE Polynucleotide tuberculosis vaccine
 JOURNAL Patent: US 5736524-A 24 07-APR-1998;
 FEATURES
 source Location/Qualifiers
 1..37
 /organism="unknown"
 BASE COUNT 5 a 12 c 13 g 7 t
 ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 37;
 Best Local Similarity 86.7%; Pred. No. 3e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaagactc 15
 |||||
 Db 7 TCTACCAAGACTC 21

RESULT 10
 LOCUS AR000593 37 bp DNA PAT 04-DEC-1998
 DEFINITION Sequence 25 from patent US 5736524.
 ACCESSION AR000593
 VERSION AR000593.1 GI:3963124
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 37)
 AUTHORS Content, J., Huygen, K., Liu, M. A., Montgomery, D. and Uimer, J.
 TITLE Polynucleotide tuberculosis vaccine
 JOURNAL Patent: US 5736524-A 25 07-APR-1998;
 FEATURES
 source Location/Qualifiers
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 BASE COUNT 6 a 11 c 10 g 10 t
 ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 37;
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 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaagactc 15
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 Db 7 TCTACCAAGACTC 21

RESULT 11
LOCUS AR05815 48 bp DNA PAT 07-SEP-2000
DEFINITION Sequence 10 from patent US 5985281.
ACCESSION AR05815
VERSION AR05815.1 GI:10012581
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 48)
Taylorson,C.John, Eggelte,H.Johannes, Tarragona-Piol,A.,
Rabin,B.Robert, Boyle,F.Thomas, Hennam,J.Frederick,
Blakey,D.Charles, Marsham,P.Robert, Heaton,D.William, Davies,D.Huw,
Slater,A.Michael and Hennequin,L.FrancoisAndre.
TITLE Chemical compounds
JOURNAL Patent: US 5985281-A 10 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..48
BASE COUNT 15 a 10 c 13 g 10 t
ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 48;
Best Local Similarity 86.7%; Pred. No. 2.9e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tctaccaagacttc 15
Db 19 tctacctgacgaattc 5

RESULT 12
LOCUS AR09164 48 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 47 from patent US 6077692.
ACCESSION AR09164
VERSION AR09164.1 GI:12808930
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 48)
Ruben,S.M., Jimenez,P., Duan,D.Roxanne, Rampy,M.A., Mendrick,D.,
Zhang,J., M.J., Moore,P.A., Coleman,T.A., Gruber,J.R., Dillon,P.J.
and Gentz,R.L.
TITLE Keratinocyte growth factor-2
JOURNAL Patent: US 6077692-A 47 20-JUN-2000;
FEATURES Location/Qualifiers
source 1..48
BASE COUNT 12 a 12 c 9 g 15 t
ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 48;
Best Local Similarity 86.7%; Pred. No. 2.9e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tctaccaagacttc 15
Db 25 ttaccacagacttc 39

RESULT 13
LOCUS AR058934 21 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5837839.
ACCESSION AR058934
VERSION AR058934.1 GI:5984511

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 21)
Toth,M.John and Huwyler,L.Robin.
TITLE DNA coding sequences for mevalonate Pyrophosphate decarboxylase
JOURNAL Patent: US 5837839-A 5 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..21
BASE COUNT 4 a 4 c 6 g 7 t
ORIGIN

Query Match 76.0%; Score 11.4; DB 6; Length 21;
Best Local Similarity 92.3%; Pred. No. 5.8e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 taccacagacttc 15
Db 17 tagcagagacttc 5

RESULT 14
LOCUS 168720 21 bp DNA PAT 04-FEB-1998
DEFINITION Sequence 22 from patent US 5677141.
ACCESSION 168720
VERSION 168720.1 GI:2830842
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 21)
Isogai,T., Fukagawa,M., Iwami,M., Aramori,I. and Kojo,H.
TITLE Process for producing 7-aminocephem compound or salts thereof
JOURNAL Patent: US 5677141-A 22 14-OCT-1997;
FEATURES Location/Qualifiers
source 1..21
BASE COUNT 5 a 6 c 7 g 3 t
ORIGIN

Query Match 76.0%; Score 11.4; DB 6; Length 21;
Best Local Similarity 92.3%; Pred. No. 5.8e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 taccacagacttc 15
Db 9 taccacagagacttc 21

RESULT 15
LOCUS AR019297 24 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 3 from patent US 5783406.
ACCESSION AR019297
VERSION AR019297.1 GI:3974411
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 24)
Schumm,J.W. and Puers,C.
TITLE Allelic leaders for short tandem repeat loci
JOURNAL Patent: US 5783406-A 3 21-JUL-1998;
FEATURES Location/Qualifiers
source 1..24
BASE COUNT 7 a 7 c 6 g 4 t
ORIGIN

Query Match 76.0%; Score 11.4; DB 6; Length 24;
Best Local Similarity 92.3%; Pred. No. 5.7e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 tctaccaaggact 13
||| |||||
Db 9 TCTGCCAAGGACT 21

Search completed: December 21, 2001, 11:34:02
Job time: 16649 sec

Wed Dec 26 11:51:12 2001

us-09-800-629a-209.sz1m50.rni

Page 1

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2001, 11:39:11 : Search time 303.16 Seconds
(Without alignments)
11.206 Million cell updates/sec

Title: US-09-800-629a-209

Perfect score: 15

Sequence: 1 tctaccaagacttc 15

Scoring table: IDENTITY_NUC
Gapop 10.0, Capext 1.0

Searched: 351203 seqs, 11323899 residues

Total number of hits satisfying chosen parameters: 495388

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA :
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4: /cgn2_6/ptodata/2/lna/6B.COMB.seq :
5: /cgn2_6/ptodata/2/lna/PCTUS.COMB.seq :
6: /cgn2_6/ptodata/2/lna/backfile1.seq :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	20	3	US-09-280-799-135
2	15	100.0	20	4	US-09-277-020-2
3	13.4	89.3	20	3	US-09-280-799-149
4	13.4	89.3	20	4	US-09-277-020-13
5	13.4	89.3	20	4	US-09-277-020-28
6	11.8	78.7	28	2	US-08-859-998-489
7	11.8	78.7	34	2	US-08-860-882A-16
8	11.8	78.7	37	1	US-08-338-992B-24
9	11.8	78.7	37	1	US-08-338-992B-25
10	11.8	78.7	48	2	US-08-860-882A-10
11	11.8	78.7	48	3	US-08-860-882A-47
12	11.4	76.0	21	1	US-08-314-309A-22
13	11.4	76.0	21	1	US-08-733-825-5
14	11.4	76.0	24	1	US-08-219-633-3
15	11.4	76.0	24	1	US-08-515-236-3
16	11.4	76.0	24	1	US-08-761-950-3
17	11.4	76.0	24	2	US-08-632-575B-33
18	11.4	76.0	24	2	US-08-687-080-156
19	11.4	76.0	24	3	US-08-933-358-12
20	11.4	76.0	24	4	US-09-327-229-5
21	11.4	76.0	24	5	PCT-US95-12608-5
22	11.4	76.0	39	3	US-08-444-644-4
23	11.4	76.0	39	3	US-08-120-365-58
24	11.4	76.0	22	4	US-09-515-039-58
25	10.8	72.0	20	3	US-09-357-070-26
26	10.8	72.0	20	3	US-09-280-799-150
27	10.8	72.0	20	4	US-09-277-020-14

28	10.8	72.0	20	4	US-09-277-020-29	Sequence 29, Appl
29	10.8	72.0	20	4	US-09-467-642-78	Sequence 78, Appl
30	10.8	72.0	21	4	US-09-262-773-38	Sequence 38, Appl
31	10.8	72.0	22	1	US-08-091-569-4	Sequence 4, Appl
32	10.8	72.0	22	1	US-08-091-569-5	Sequence 5, Appl
33	10.8	72.0	22	1	US-08-203-676-4	Sequence 4, Appl
34	10.8	72.0	22	1	US-08-203-676-5	Sequence 5, Appl
35	10.8	72.0	22	1	US-08-295-676A-10	Sequence 10, Appl
36	10.8	72.0	22	2	US-08-948-591-10	Sequence 10, Appl
37	10.8	72.0	22	2	US-08-822-238-4	Sequence 4, Appl
38	10.8	72.0	22	2	US-08-822-238-5	Sequence 5, Appl
39	10.8	72.0	23	3	US-09-120-887-8	Sequence 8, Appl
40	10.8	72.0	31	1	US-08-390-850-208	Sequence 208, App
41	10.8	72.0	31	1	US-08-390-850-209	Sequence 209, App
42	10.8	72.0	31	1	US-08-390-850-210	Sequence 210, App
43	10.8	72.0	31	1	US-08-390-850-211	Sequence 211, App
44	10.8	72.0	31	1	US-08-435-634-208	Sequence 208, App
45	10.8	72.0	31	1	US-08-435-634-209	Sequence 209, App

ALIGNMENTS

RESULT 1
US-09-280-799-135 : Application US/09280799
Patent No. 6136603
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: McRay, Robert
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
FILE REFERENCE: ISPH-0340
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 135
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-280-799-135

Query Match 100.0%; Score 15; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctaccaagacttc 15
Db 6 tctaccaagacttc 20

RESULT 2
US-09-277-020-2 : Application US/09277020
Patent No. 6210892
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
FILE REFERENCE: ISPH-0339
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 20

For Smith
BM

down + have
publidy to parents

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-277-020-2

Query Match 100.0%; Score 15; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctaccaagagcttc 15
|||||
DB 6 tctaccaagagcttc 20

RESULT 3
US-09-280-799-149
Sequence 149, Application US/09280799
Patent No. 6136603
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Karras, James G.
APPLICANT: McKay, Robert
TITLE OF INVENTION: TRANSDUCTION OF INTERLEUKIN-5 SIGNAL
FILE REFERENCE: ISPH-0340
CURRENT APPLICATION NUMBER: US/09/280,799
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 149
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-280-799-149

Query Match 89.3%; Score 13.4; DB 3; Length 20;
Best Local Similarity 93.3%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctaccaagagcttc 15
|||||
DB 6 tctaccaagagcttc 20

RESULT 4
US-09-277-020-13
Sequence 13, Application US/09277020
Patent No. 6210892
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
FILE REFERENCE: ISPH-0339
CURRENT APPLICATION NUMBER: US/09/277,020
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-277-020-13

Query Match 89.3%; Score 13.4; DB 4; Length 20;
Best Local Similarity 93.3%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctaccaagagcttc 15
|||||
DB 6 tctaccaagagcttc 20

RESULT 5
US-09-277-020-28
Sequence 28, Application US/09277020
Patent No. 6210892
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
FILE REFERENCE: ISPH-0339
CURRENT APPLICATION NUMBER: US/09/277,020
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-277-020-28

Query Match 89.3%; Score 13.4; DB 4; Length 20;
Best Local Similarity 93.3%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctaccaagagcttc 15
|||||
DB 6 tctaccaagagcttc 20

RESULT 6
US-08-859-998-489/c
Sequence 489, Application US/08859998
Patent No. 5994076
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Jokhadze, George
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 489:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-489

Query Match 78.7%; Score 11.8; DB 2; Length 28;
Best Local Similarity 86.7%; Pred. No. 2.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaaggacttc 15
||||| ||| ||
Db 21 TCTACCAAGGACTTC 7

RESULT 7
US-08-860-882A-16/c
Sequence 16, Application US/08860882A
Patent No. 5985281
GENERAL INFORMATION:
APPLICANT: TAYLORSON, CHRISTOPHER JOHN
APPLICANT: EGGELTE, HENDRIKUS JOHANNES
APPLICANT: TARRAGONA-FLOL, ANTONIO
APPLICANT: RABIN, BRIAN ROBERT
APPLICANT: BOYLE, FRANCIS THOMAS
APPLICANT: HENNAM, JOHN FREDERICK
APPLICANT: BLAKELY, DAVID CHARLES
APPLICANT: MARSHAM, PETER ROBERT
APPLICANT: HEATON, DAVID WILLIAM
APPLICANT: DAVIES, DAVID HUV
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,882A
FILING DATE: JUNE 23, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DONALD J. BIRD
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 9901/238653
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3027
TELEFAX: (202) 822-0944
TELEX: 6174627 CUSH
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 bases
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
US-08-860-882A-16

Query Match 78.7%; Score 11.8; DB 2; Length 34;
Best Local Similarity 86.7%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaaggacttc 15
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Db 19 TCTACCTAGGACTTC 5

RESULT 8
US-08-338-992B-24
Sequence 24, Application US/08338992B
Patent No. 5736524
GENERAL INFORMATION:
APPLICANT: CONTENT, JEAN
APPLICANT: HUYGEN, KRIS
APPLICANT: LIU, MARGARET A.
APPLICANT: MONTGOMERY, DONNA
APPLICANT: ULMER, JEFFREY
TITLE OF INVENTION: A POLYNUCLEOTIDE TUBERCULOSIS VACCINE
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MICHAEL D. YABLONSKY - MERCK & CO., INC.
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,992B
FILING DATE: 14-NOV-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: YABLONSKY, MICHAEL D.
REGISTRATION NUMBER: 40,407
REFERENCE/DOCKET NUMBER: 19342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-4678
TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-338-992B-24

Query Match 78.7%; Score 11.8; DB 1; Length 37;
Best Local Similarity 86.7%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctaccaaggacttc 15
||||| ||| |||
Db 7 TCTACCATGGCTTC 21

RESULT 9
US-08-338-992B-25
Sequence 25, Application US/08338992B
Patent No. 5736524
GENERAL INFORMATION:
APPLICANT: CONTENT, JEAN

APPLICANT: HUYGEN, KRIS
APPLICANT: LIU, MARGARET A.
APPLICANT: MONTGOMERY, DONNA
APPLICANT: ULMER, JEFFREY
TITLE OF INVENTION: A POLYNUCLEOTIDE TUBERCULOSIS VACCINE
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MICHAEL D. YABLONSKY - MERCK & CO., INC.
STREET: 126 E. LINCOLN AVE., - P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,992B
FILING DATE: 14-NOV-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: YABLONSKY, MICHAEL D.
REGISTRATION NUMBER: 40,407
REFERENCE/DOCKET NUMBER: 19342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-4678
TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-338-992B-25

Query Match 78.7%: Score 11.8; DB 1; Length 37;
Best Local Similarity 86.7%: Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1 tctaccaagagcttc 15
Db 7 TCTACCATGGCCTTC 21
|||||'|||

RESULT 10
US-08-860-882A-10/c
Sequence 10, Application US/08860882A
Patent No. 5985281
GENERAL INFORMATION:
APPLICANT: TAYLORSON, CHRISTOPHER JOHN
APPLICANT: EGGELITE, HENDRIKUS JOHANNES
APPLICANT: TARRAGONA-PTOL, ANTONIO
APPLICANT: RABIN, BRIAN ROBERT
APPLICANT: BOYLE, FRANCIS THOMAS
APPLICANT: HENNAM, JOHN FREDERICK
APPLICANT: BLAKELY, DAVID CHARLES
APPLICANT: MARSHAM, PETER ROBERT
APPLICANT: HEATON, DAVID WILLIAM
APPLICANT: DAVIES, DAVID HUW
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,882A
FILING DATE: JUNE 23, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DONALD J. BIRD
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 9901/238653
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3027
TELEFAX: (202) 822-0944
TELEX: 6174627 CUSH
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-860-882A-10

Query Match 78.7%: Score 11.8; DB 2; Length 48;
Best Local Similarity 86.7%: Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1 tctaccaagagcttc 15
Db 19 TCTACTAGCAATTC 5
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RESULT 11
US-09-023-082A-47
Sequence 47, Application US/09023082A
Patent No. 6077692
GENERAL INFORMATION:
APPLICANT: RUBEN, STEVEN M.
APPLICANT: JIMENEZ, PABLO
APPLICANT: DUAN, D. ROXANNE
APPLICANT: RAMPEY, MARK A.
APPLICANT: MENDRICK, DONNA
APPLICANT: ZHANG, JUN
APPLICANT: NI, JIAN
APPLICANT: MOORE, PAUL A.
APPLICANT: COLEMAN, TIMOTHY A.
APPLICANT: GRUBER, JOACHIM R.
APPLICANT: DILLON, PATRICK J.
APPLICANT: GENTZ, REINER L.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,082A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01790
FILING DATE: 14-FEB-1995
PRIOR APPLICATION DATA:

RESULT 13
 US-08-733-825-5/c
 Sequence 5, Application US/08733825
 Patent No. 5837839
 GENERAL INFORMATION:
 APPLICANT: Toth, Matthew J.
 APPLICANT: Hawley, Leslie R.
 TITLE OF INVENTION: Coding Sequences for Mevalonate
 TITLE OF INVENTION: Pyrophosphate Decarboxylase
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 5837839artis Patent and Trademark Department
 STREET: 59 Route 10
 CITY: East Hanover
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07936-1080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/733,825
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/005,652
 FILING DATE: 18-OCT-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5837839ak, Henry P.
 REGISTRATION NUMBER: 33200
 REFERENCE/DOCKET NUMBER: 4-20615/P1/CGC 1834
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 277-5110
 TELEFAX: (908) 277-4606
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

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